

FIG.1A

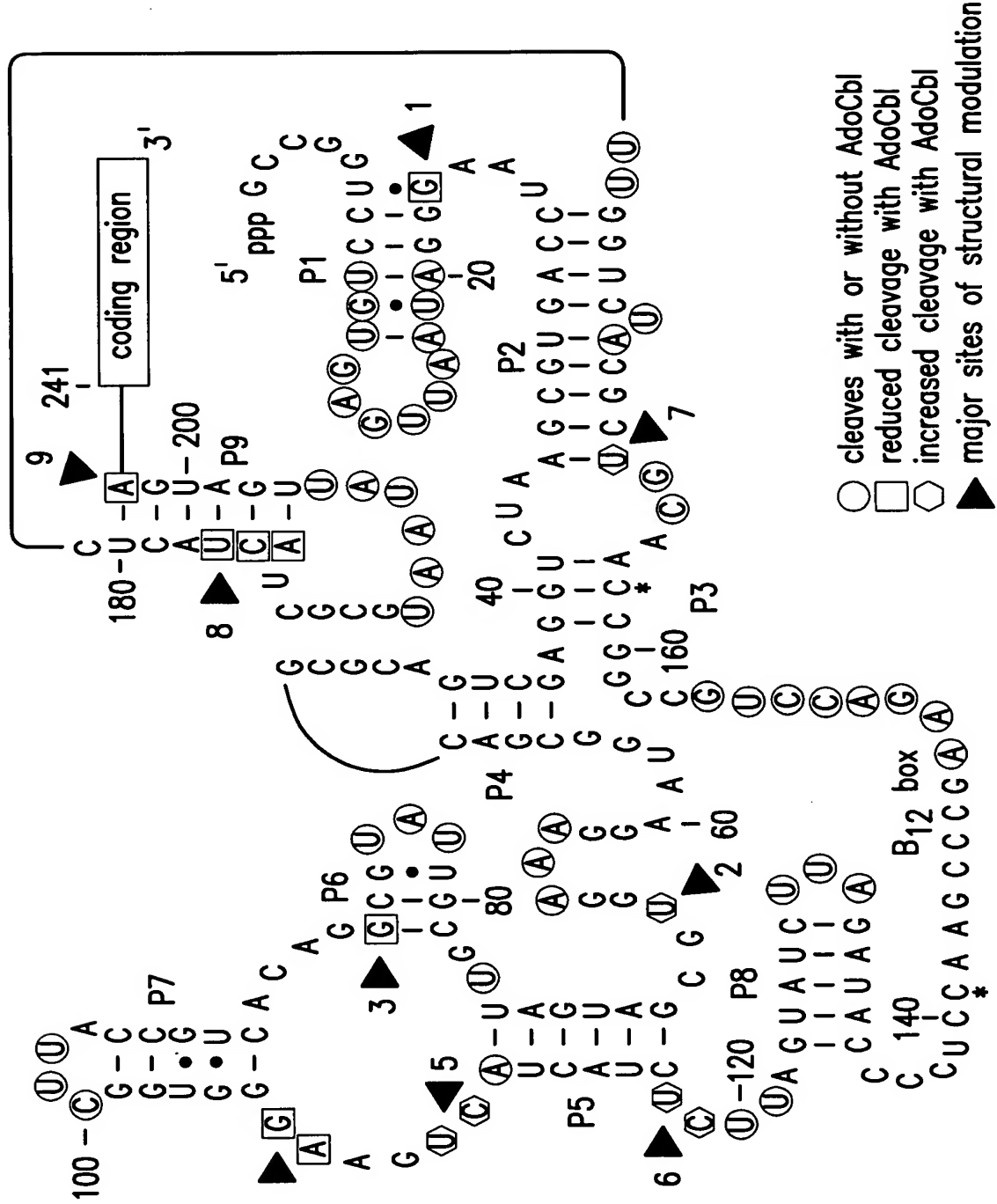


FIG. 1B

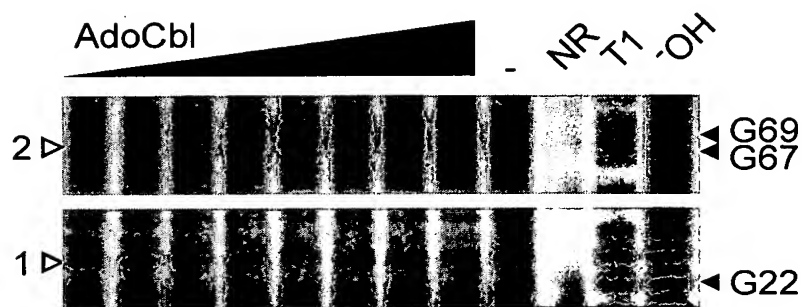


FIG.2A

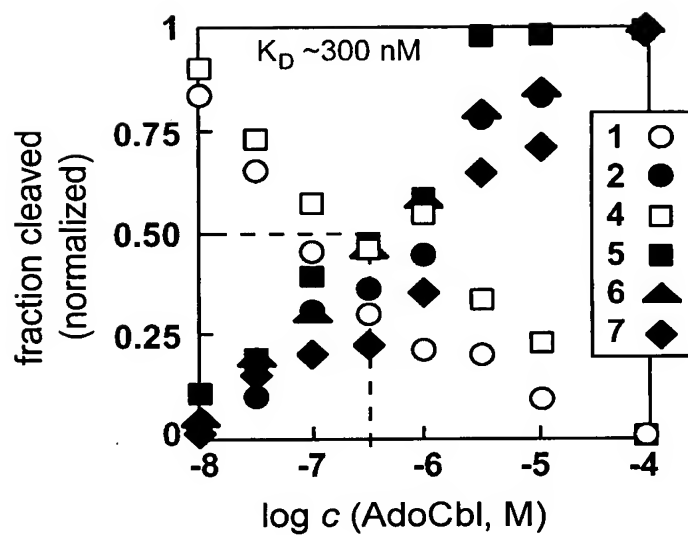


FIG.2B

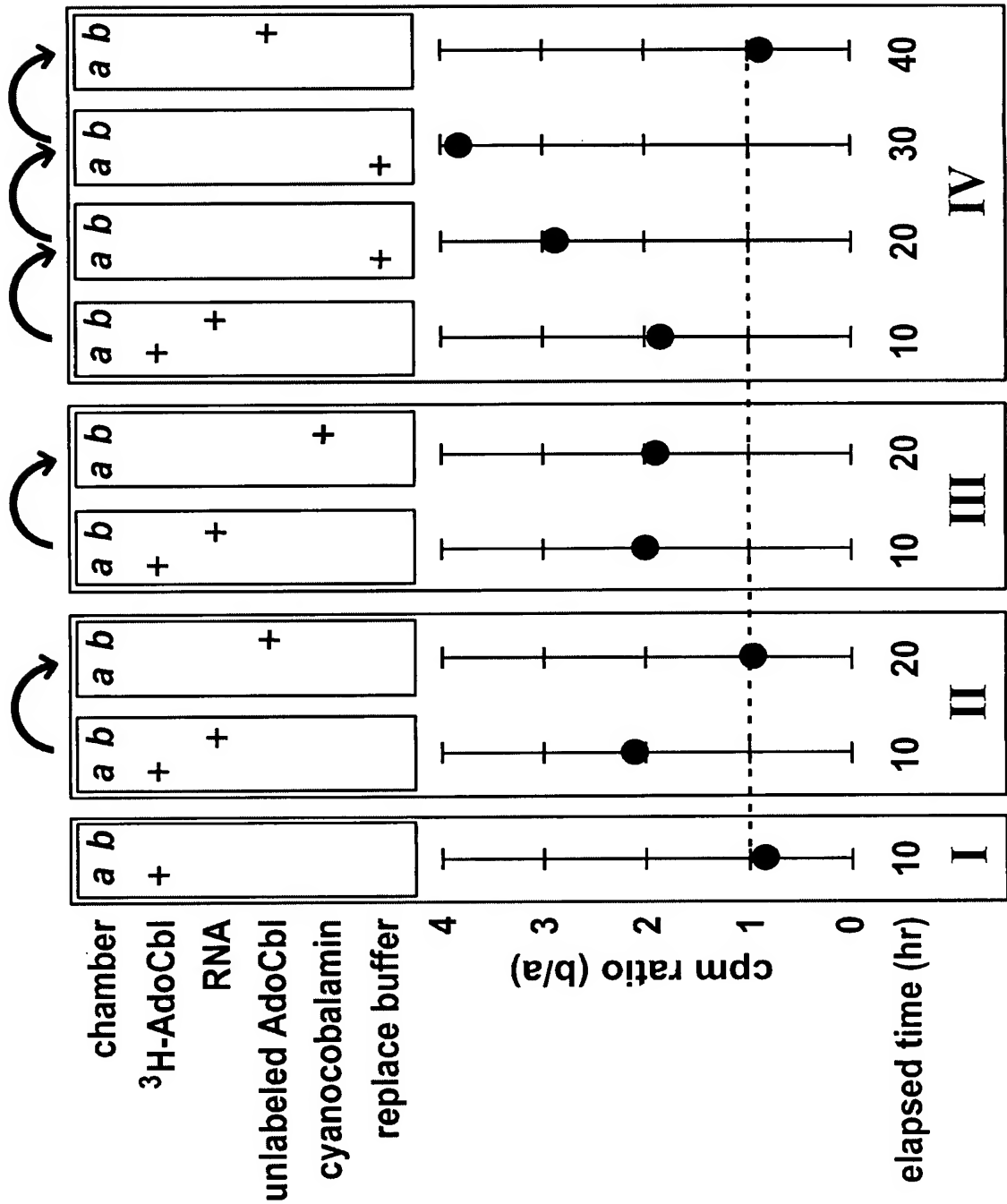


FIG.3



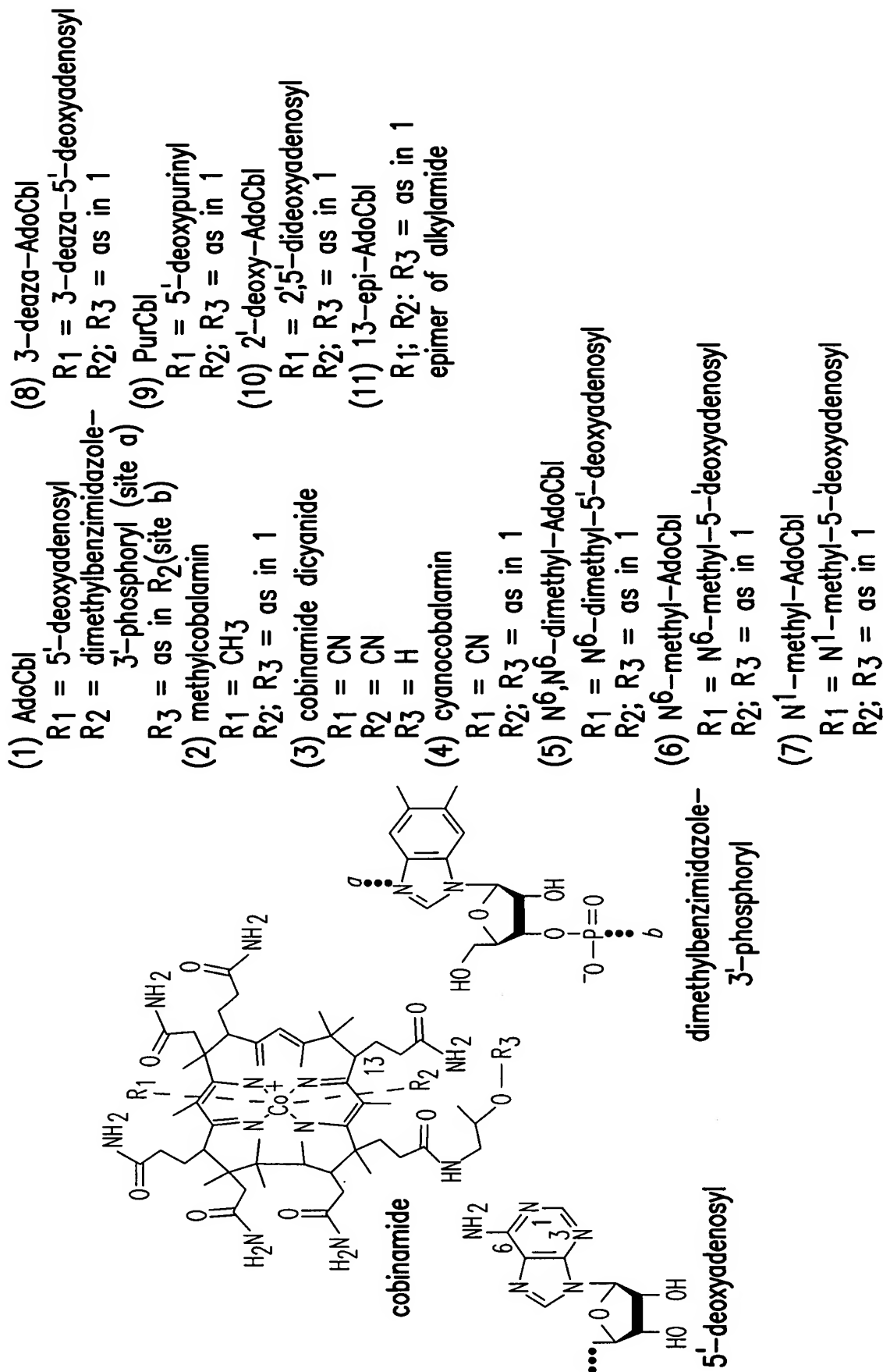


FIG. 4A

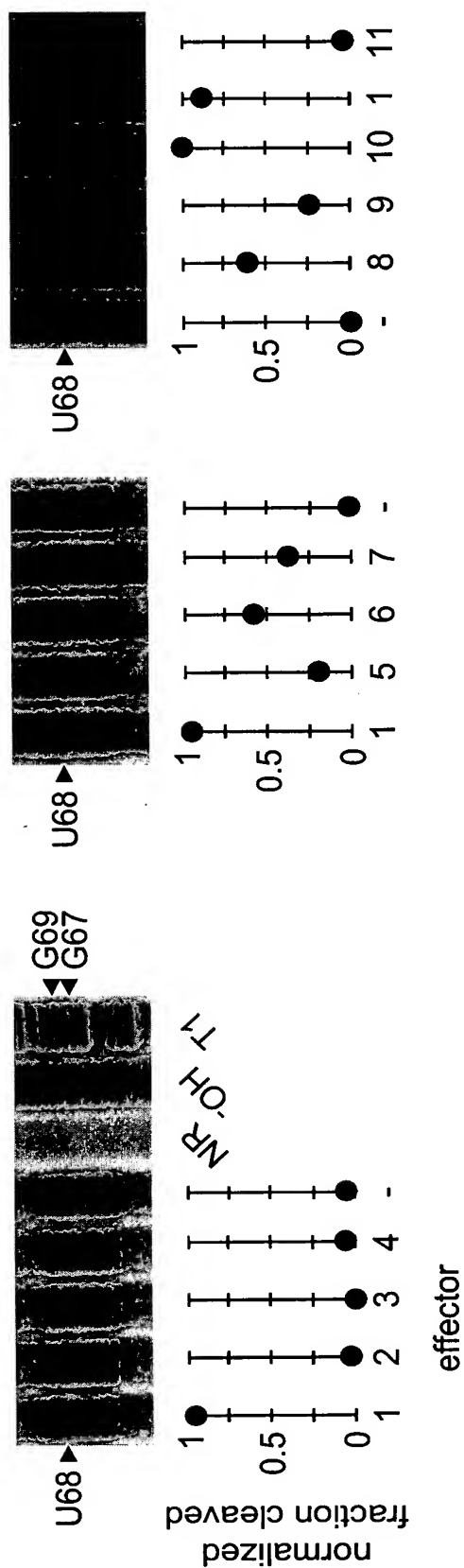


FIG. 4B

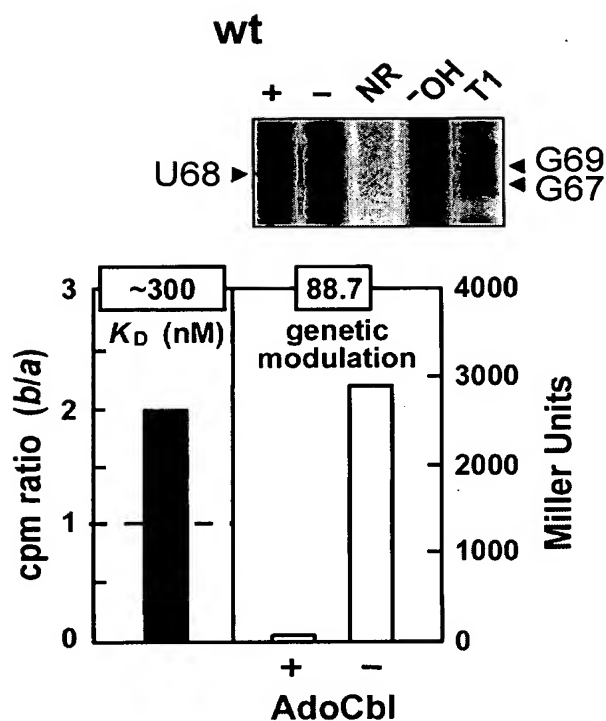


FIG.5A

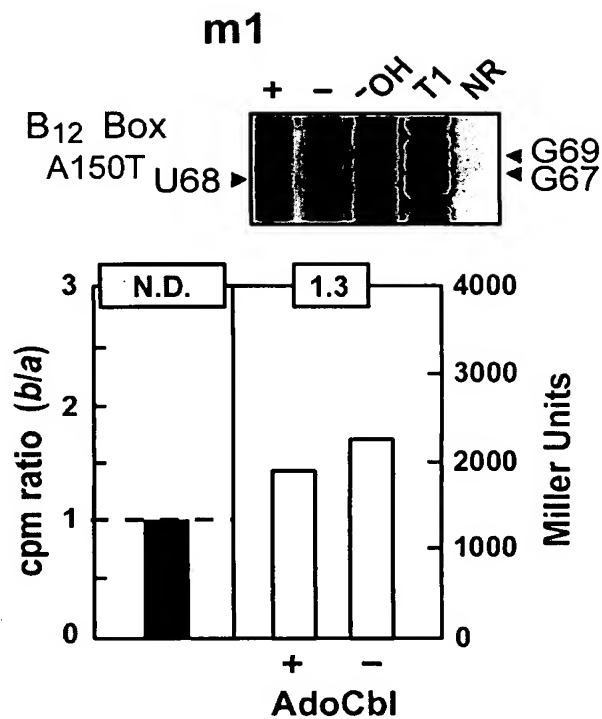


FIG.5B

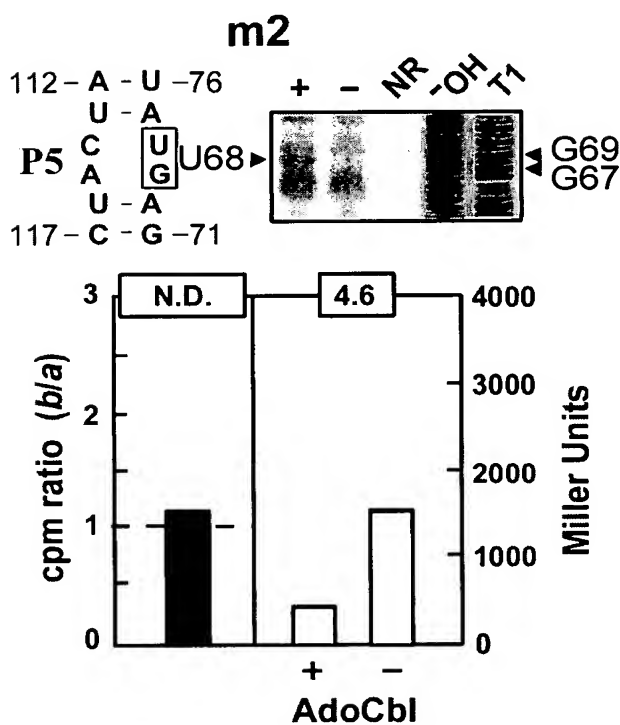


FIG.5C

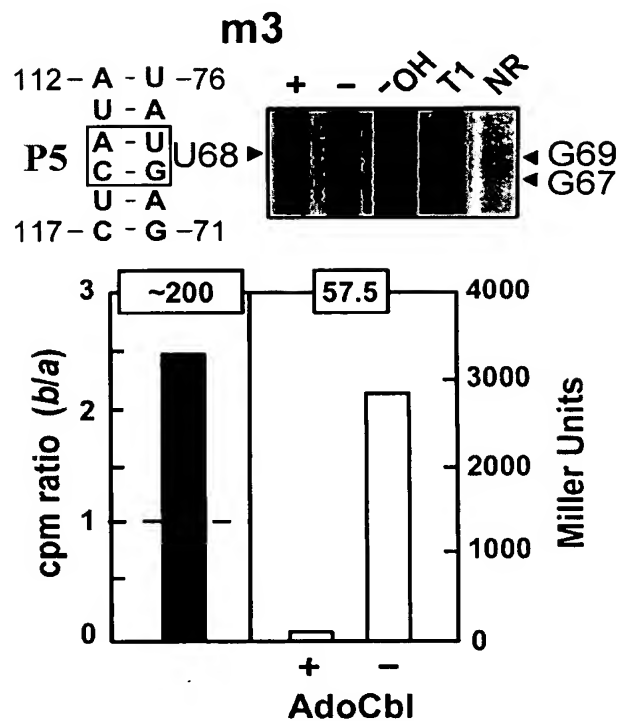


FIG.5D

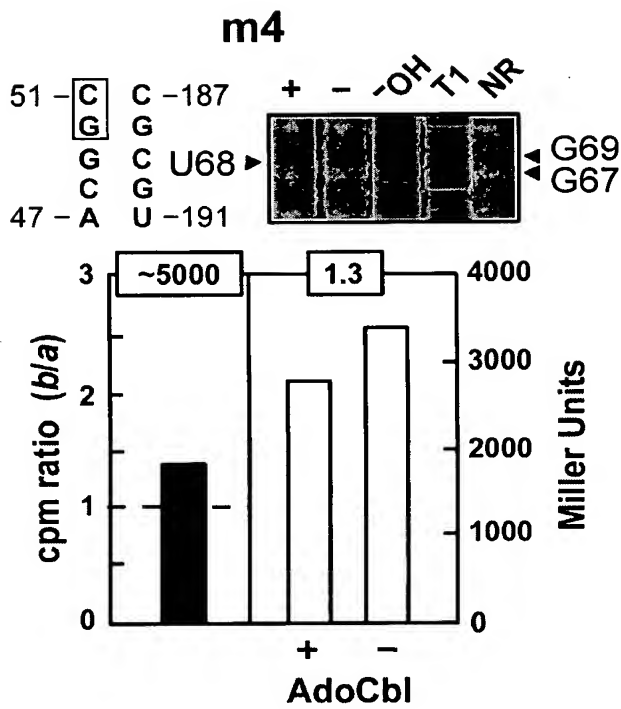


FIG.5E

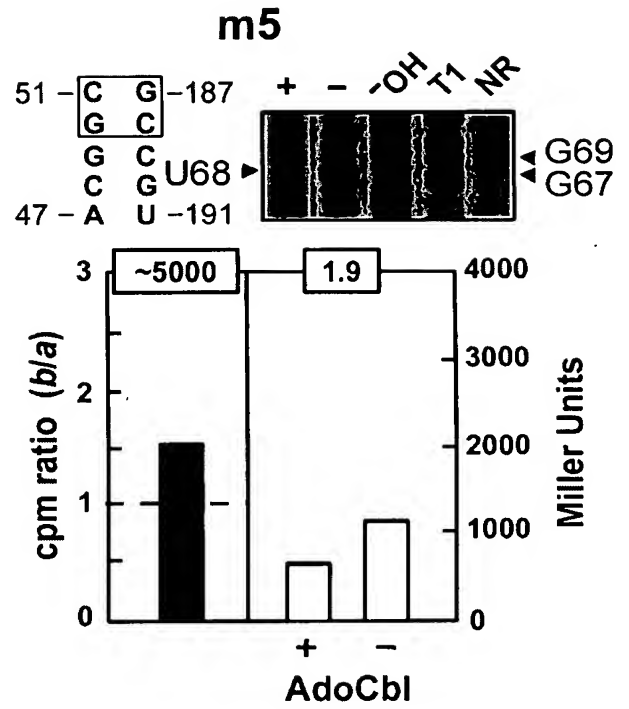


FIG.5F

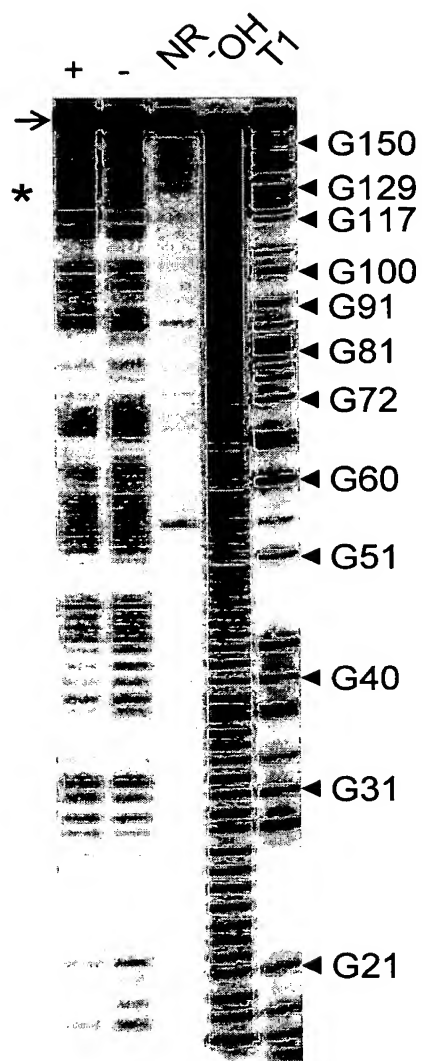


FIG. 6A

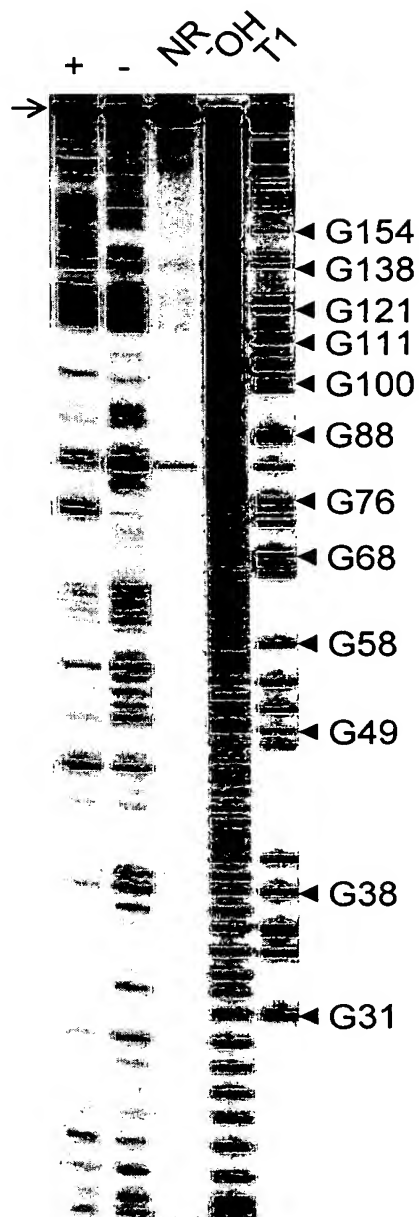


FIG. 6C

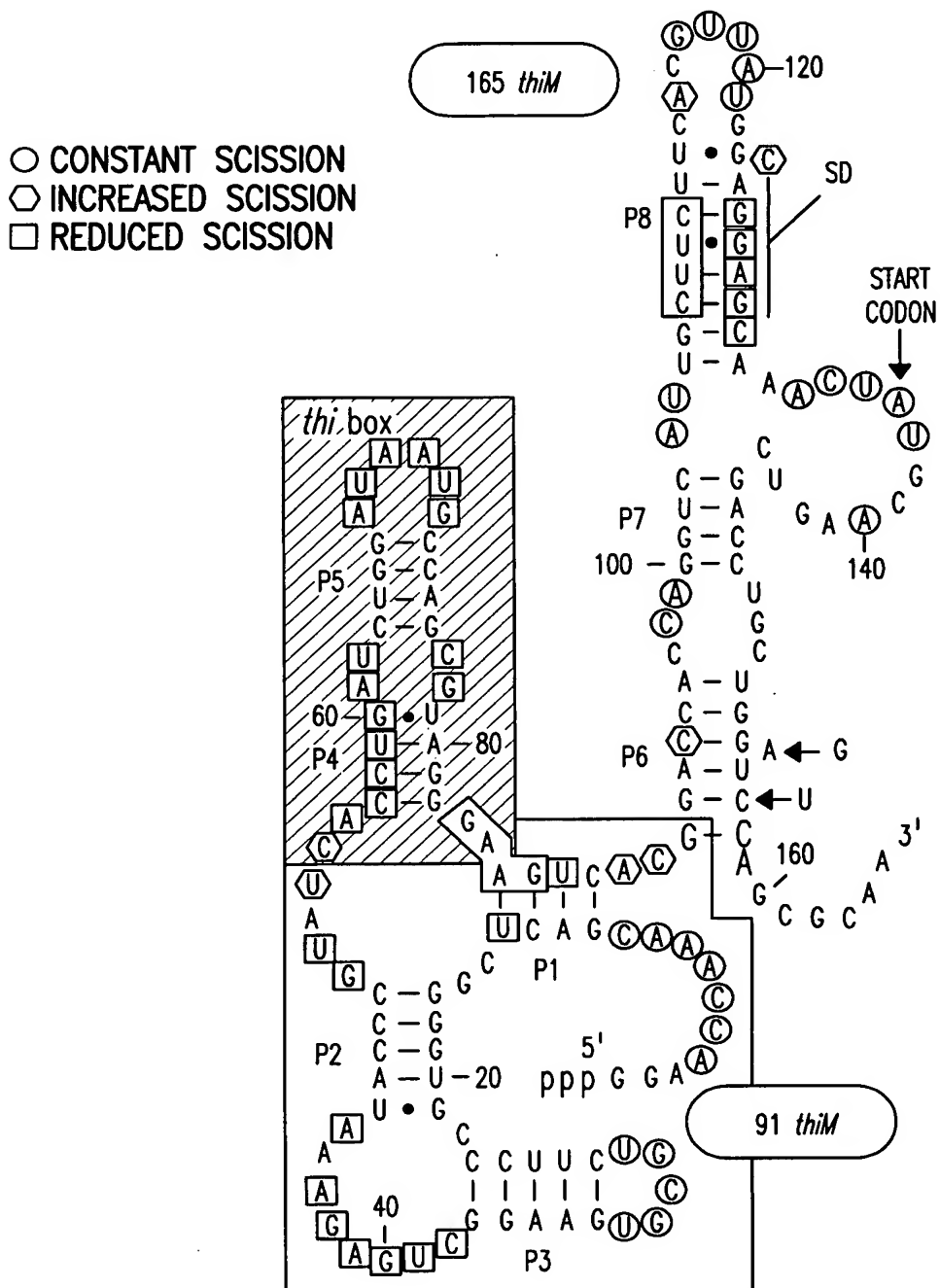


FIG.6B

- CONSTANT SCISSION
- ◊ INCREASED SCISSION
- REDUCED SCISSION

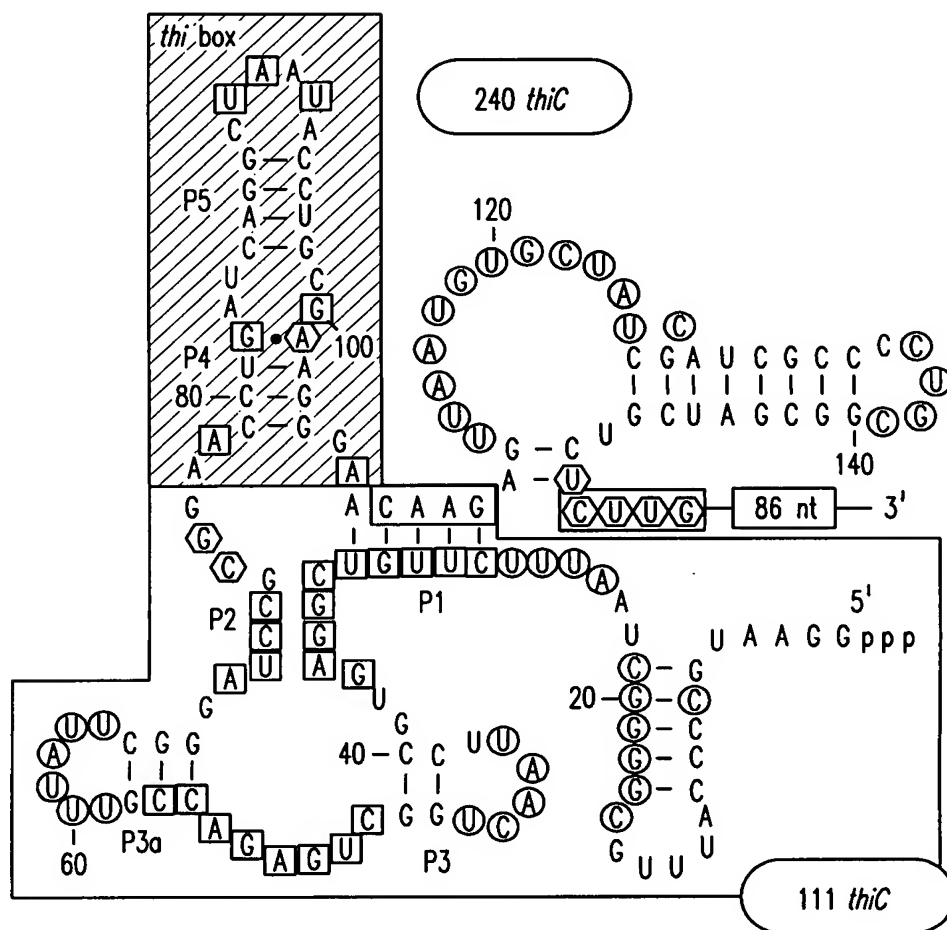


FIG.6D

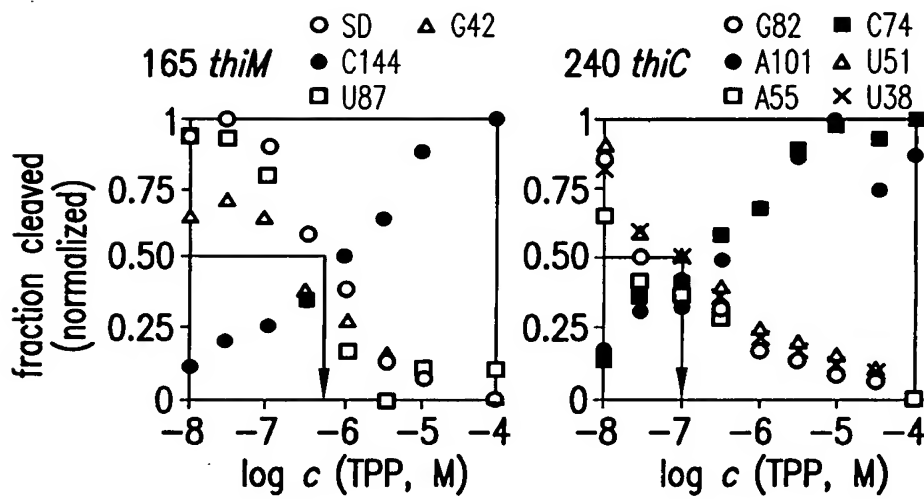


FIG. 7A

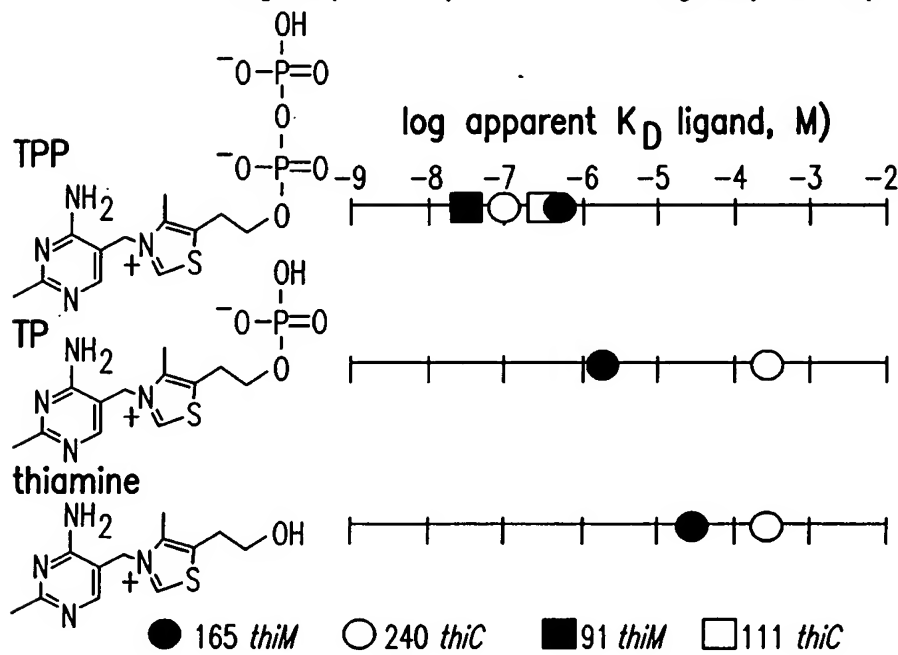


FIG. 7B

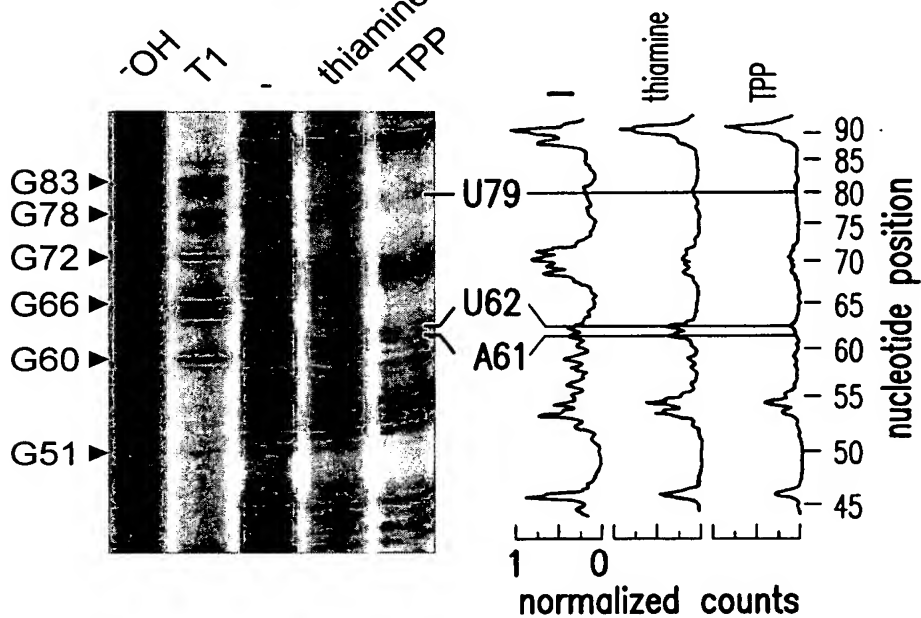


FIG. 7C



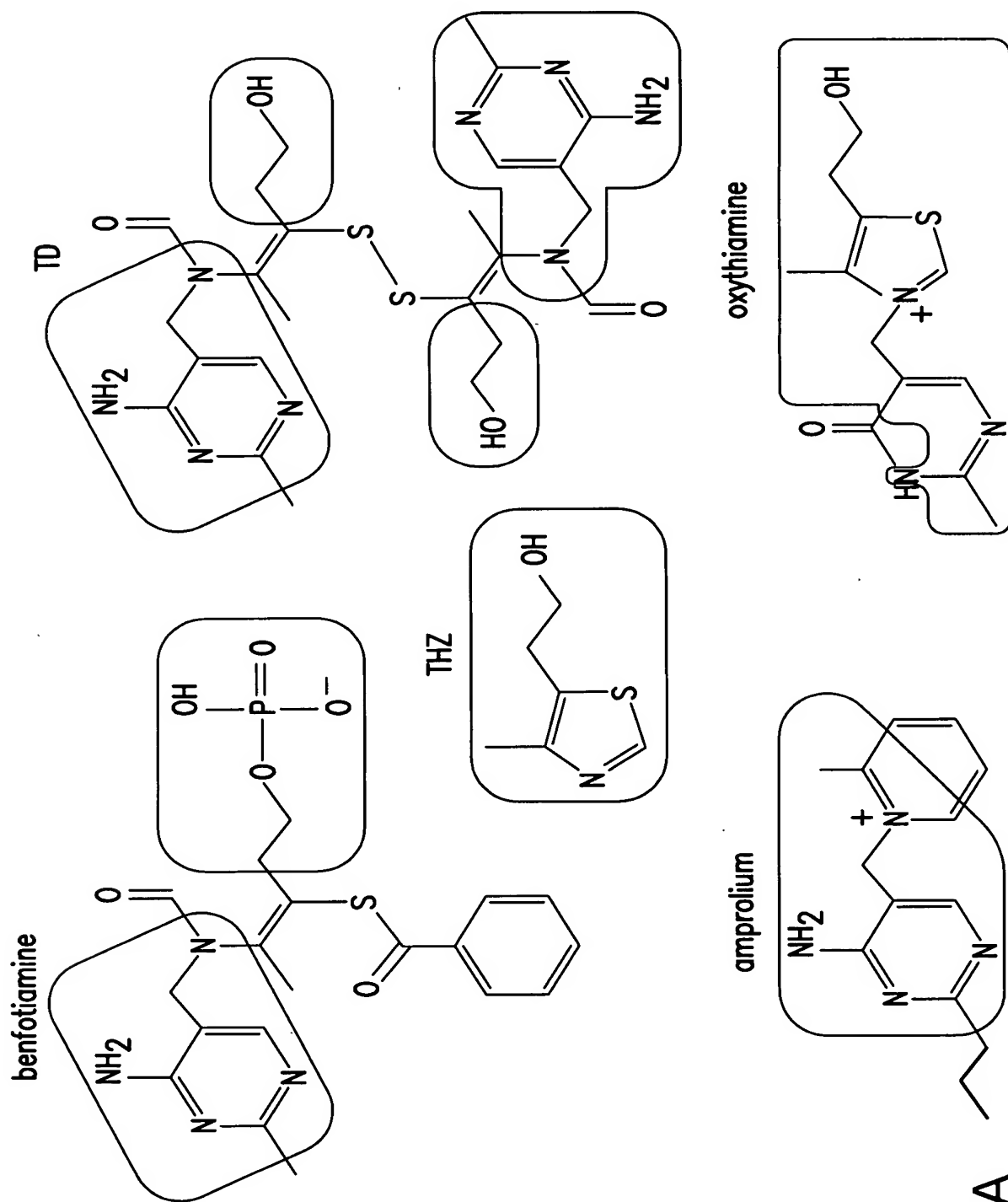


FIG. 8A

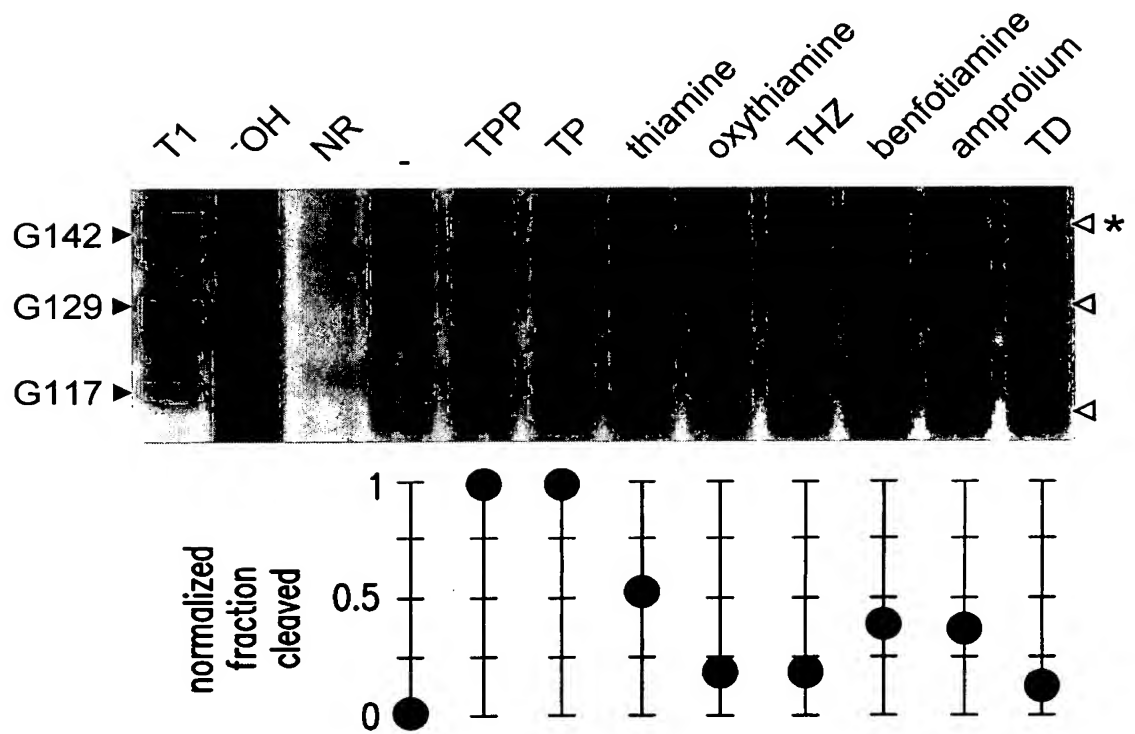
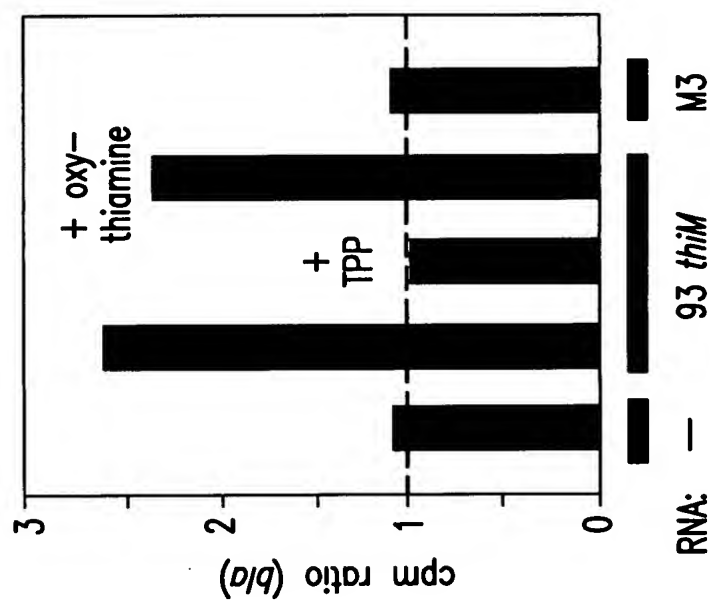


FIG.8B



**FIG. 8D**

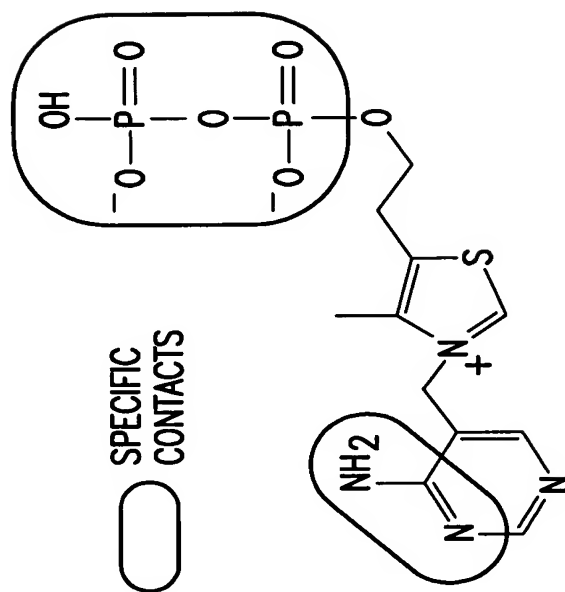


FIG. 8C

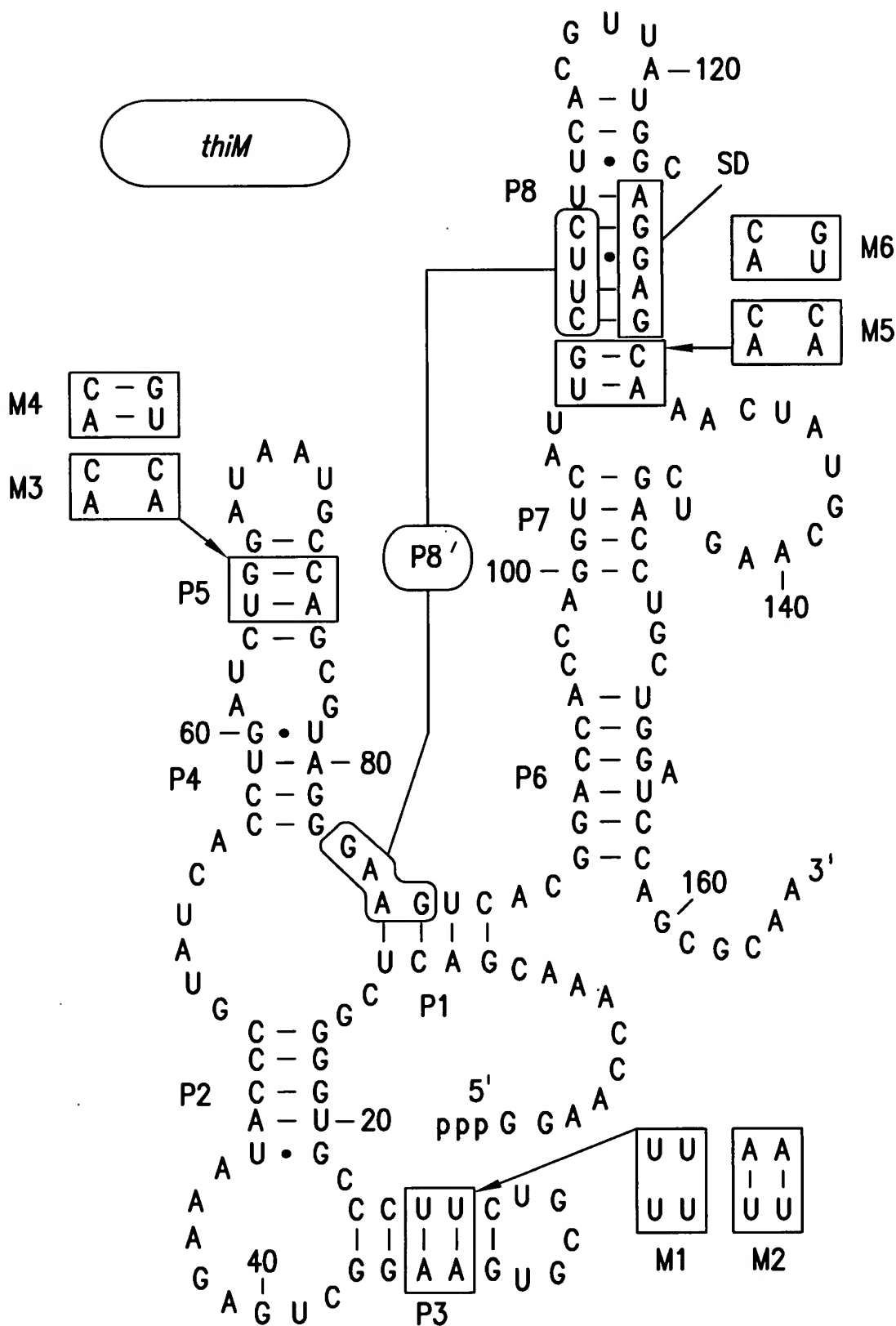


FIG.9A

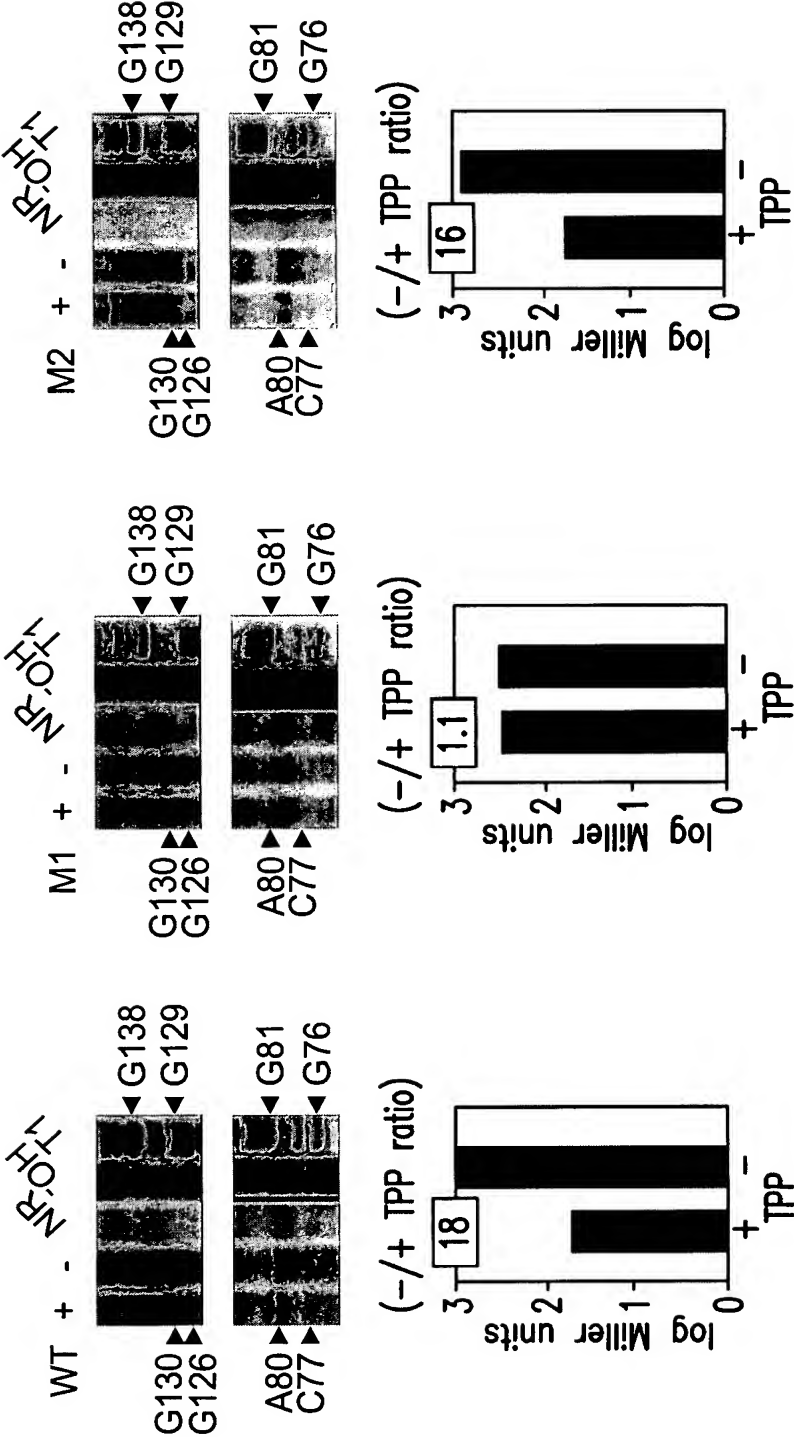


FIG. 9B-1

mutant	TPP binding	SD status (+ TPP)	genetic modulation (-/+ TPP ratio)
WT	yes	closes	18
M1	no	unchanged	1.1
M2	yes	closes	16
M3	no	unchanged	1.1
M4	yes	closes	4.8
M5	no	unchanged	2.1
M6	yes	n.d.	10
M7	yes	n.d.	4.1
M8	yes	n.d.	1.6
M9	yes	n.d.	2.4

FIG.9B-2

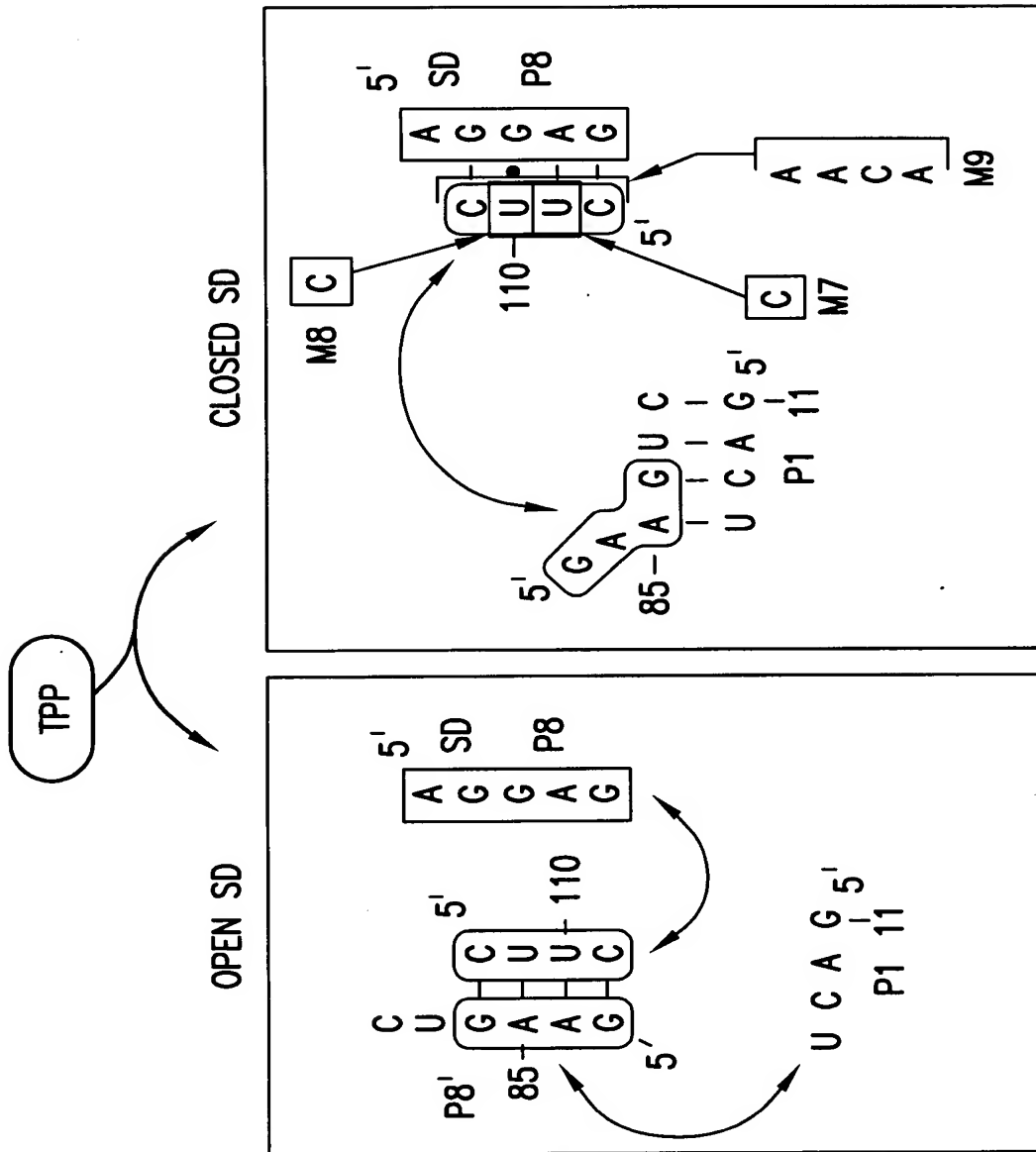
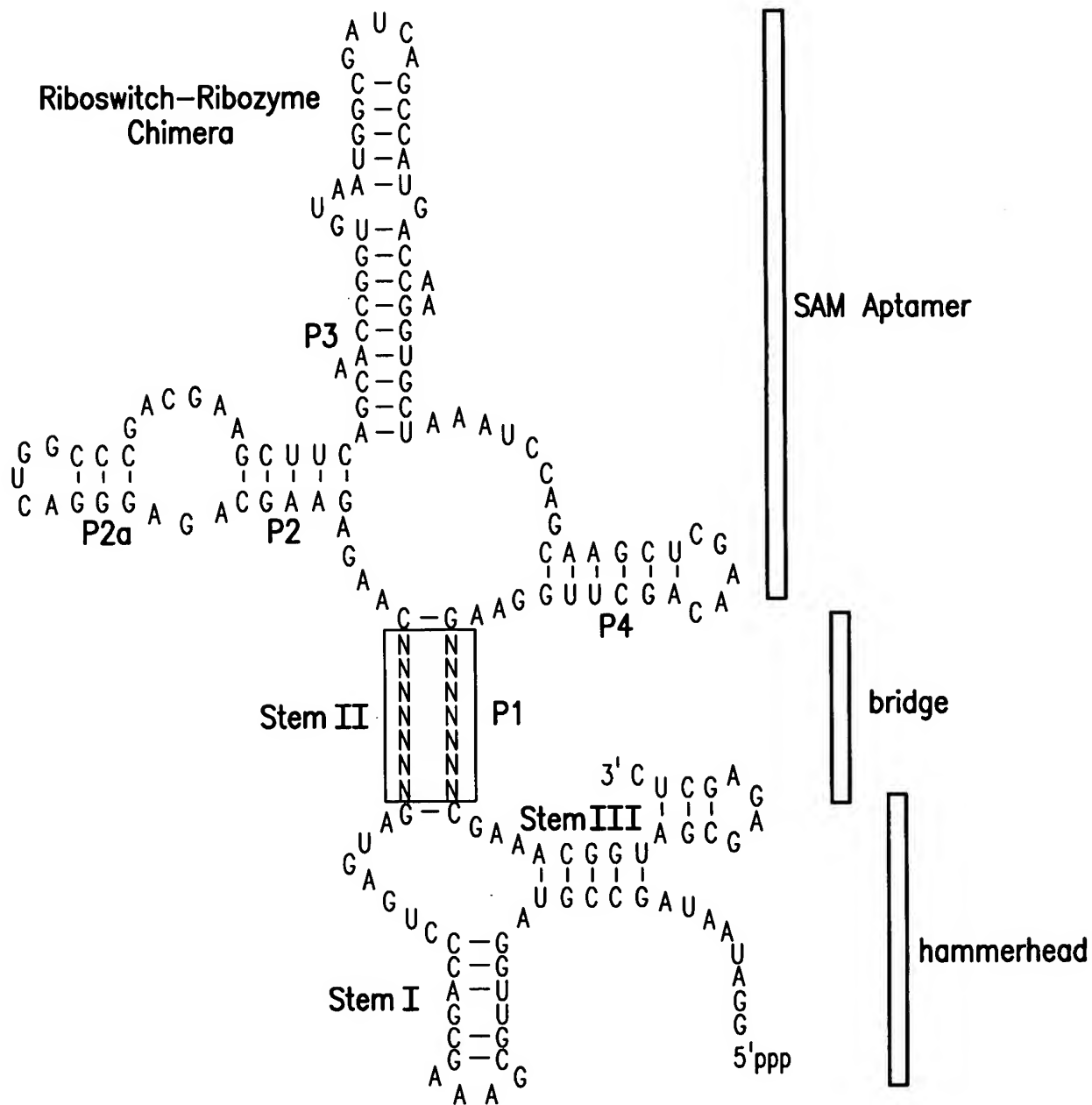


FIG.9C



**FIG.10**



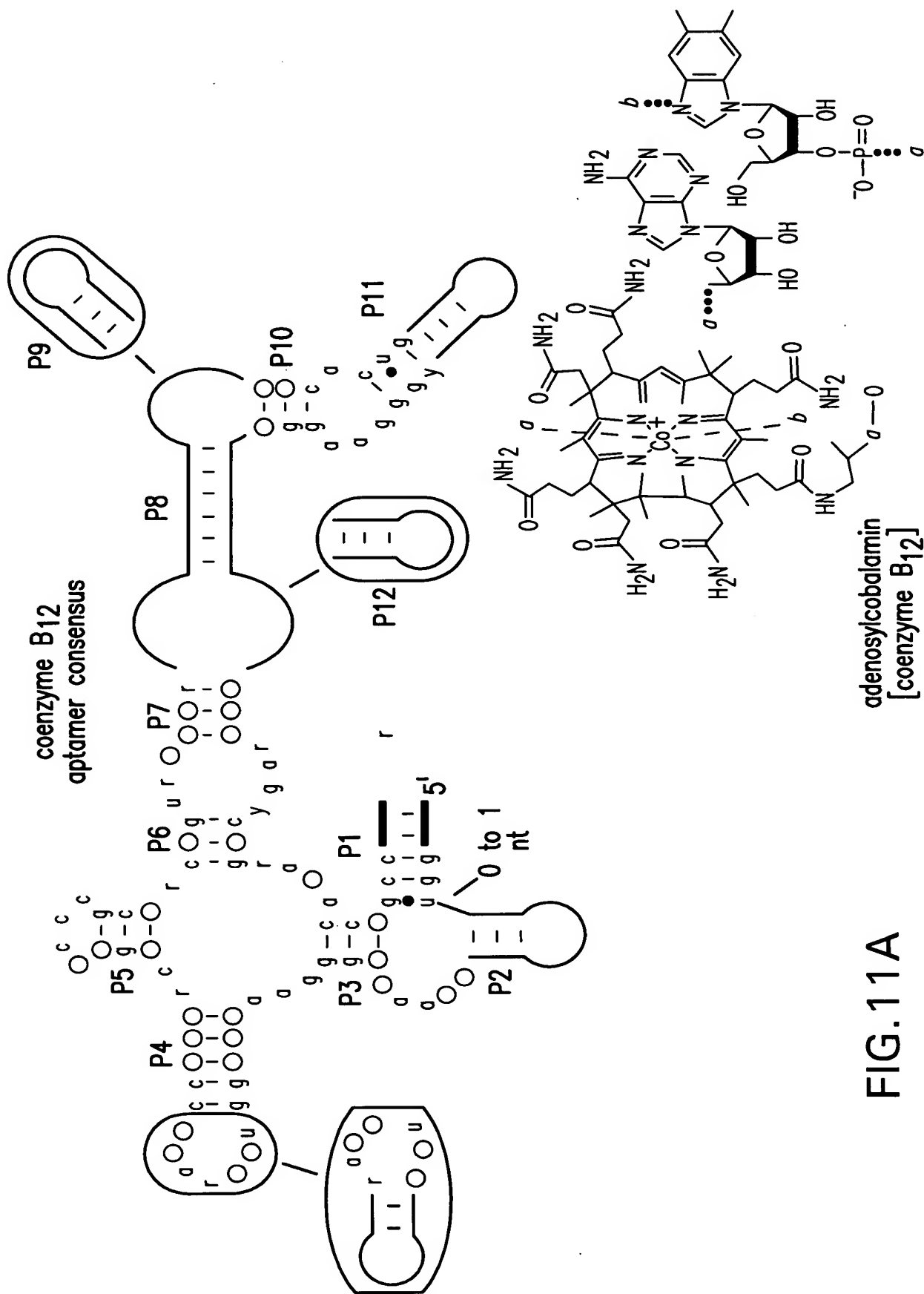


FIG. 11A

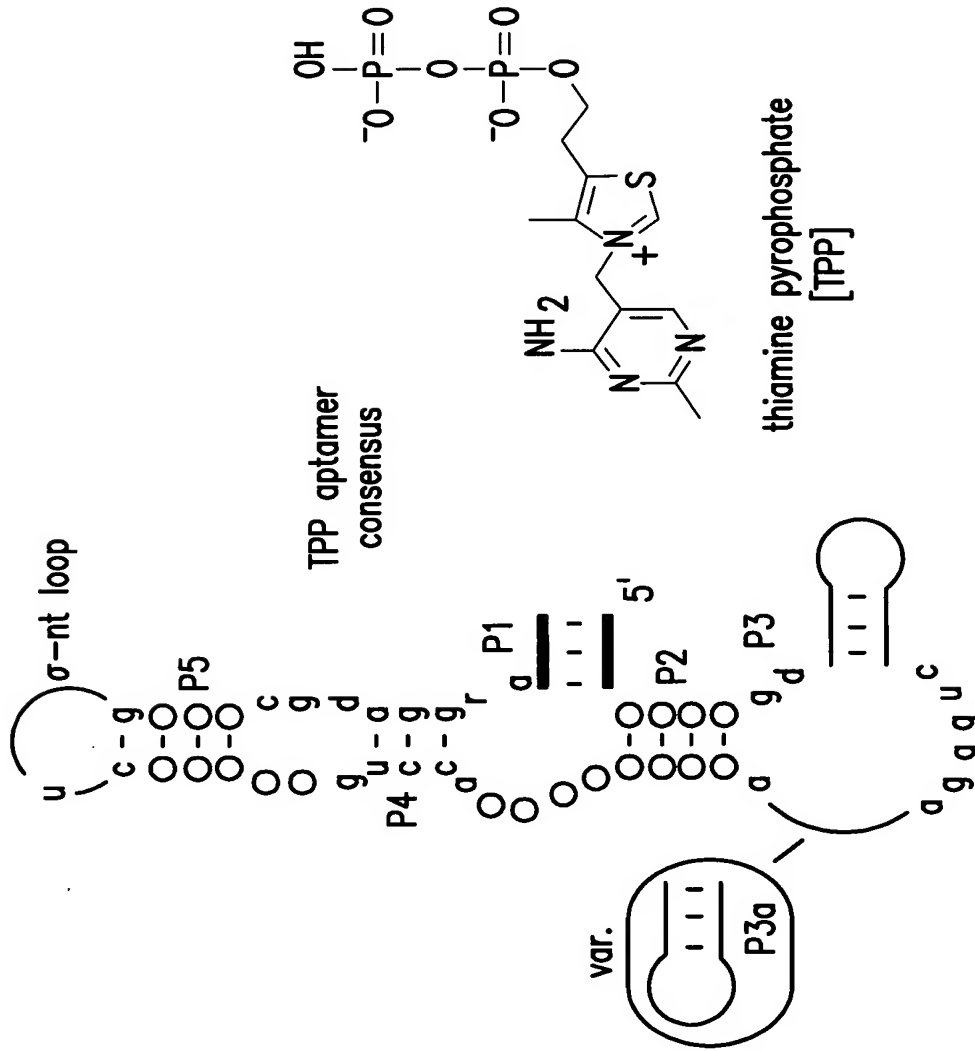


FIG. 11B

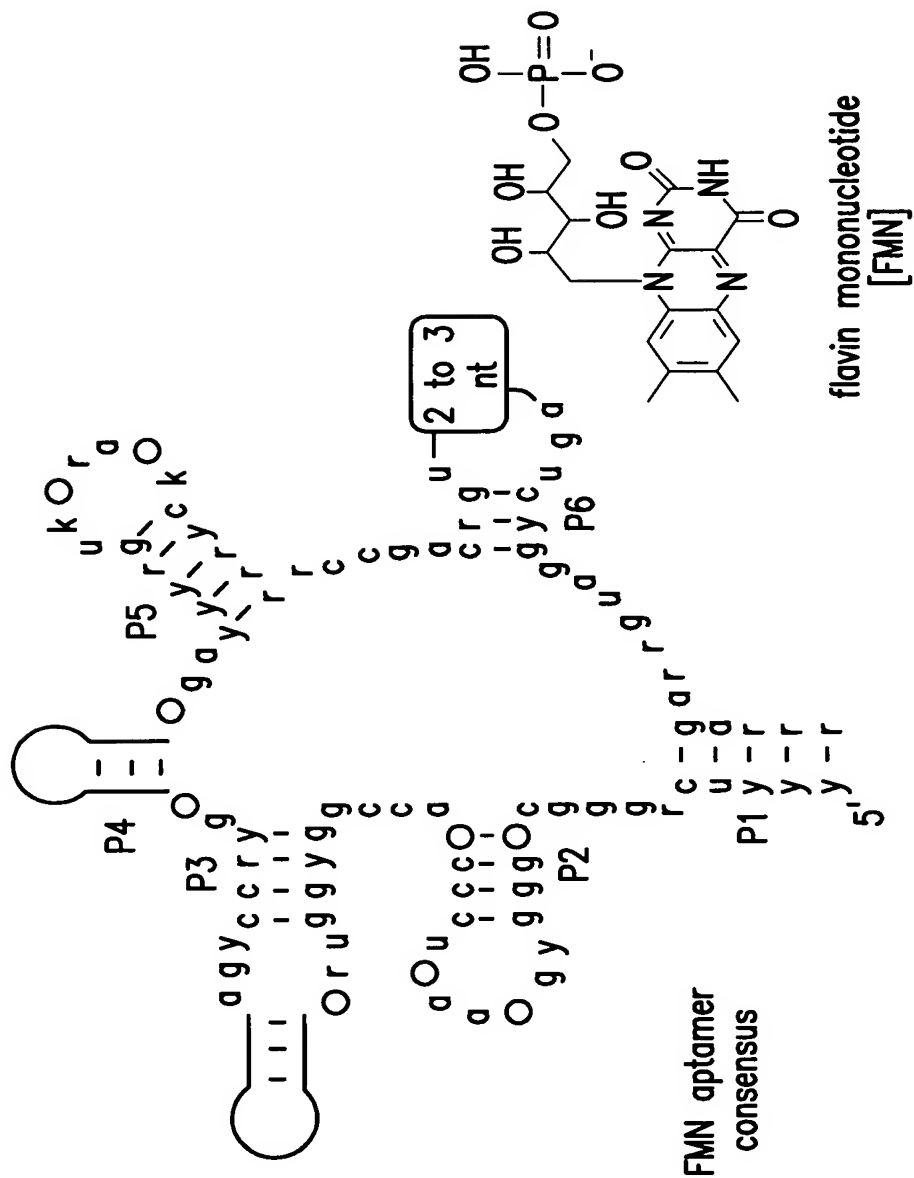


FIG.11C

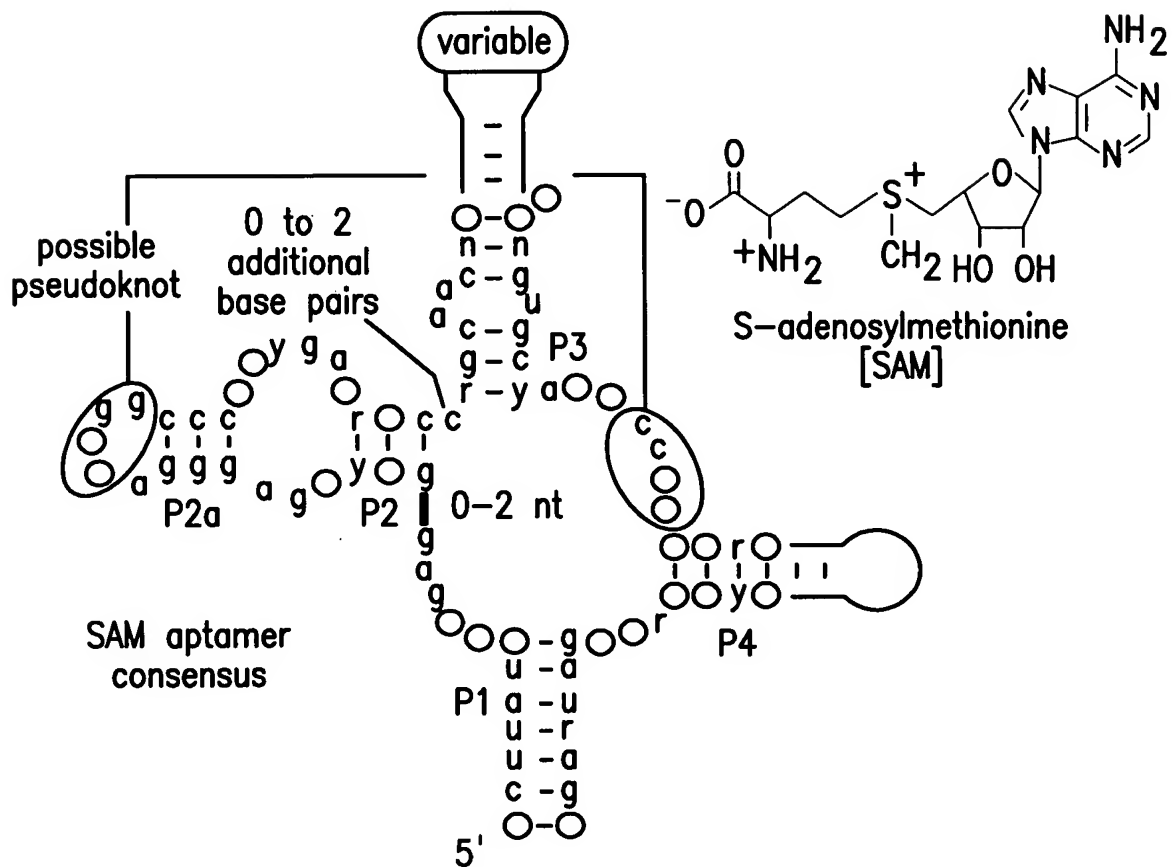


FIG. 11D

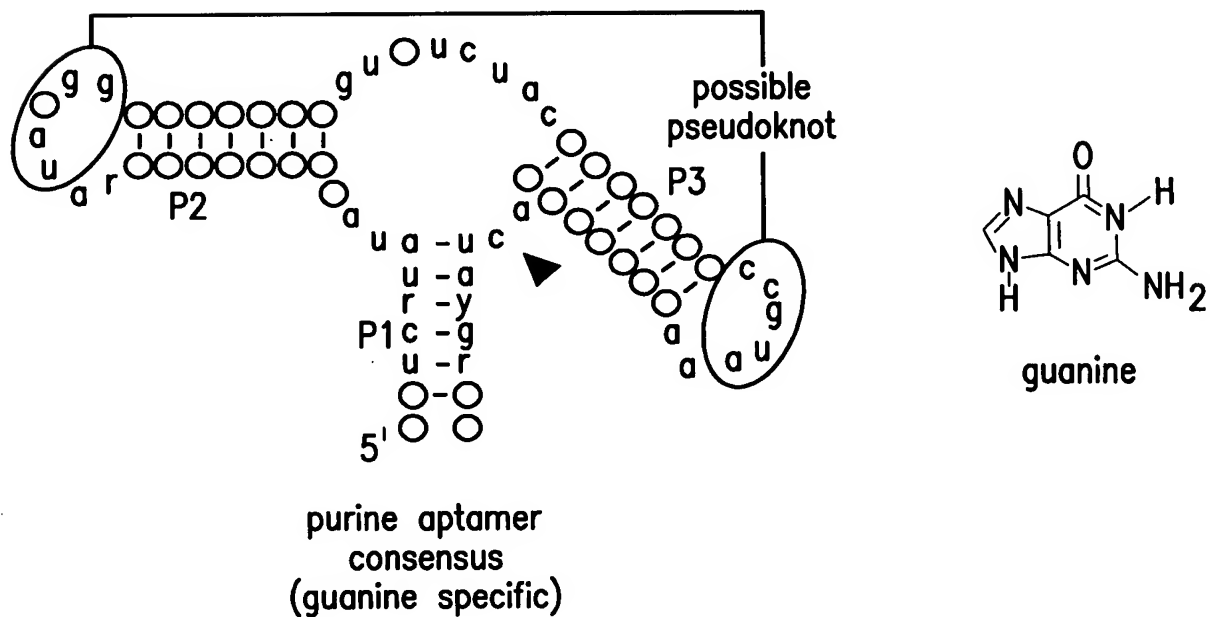


FIG. 11E

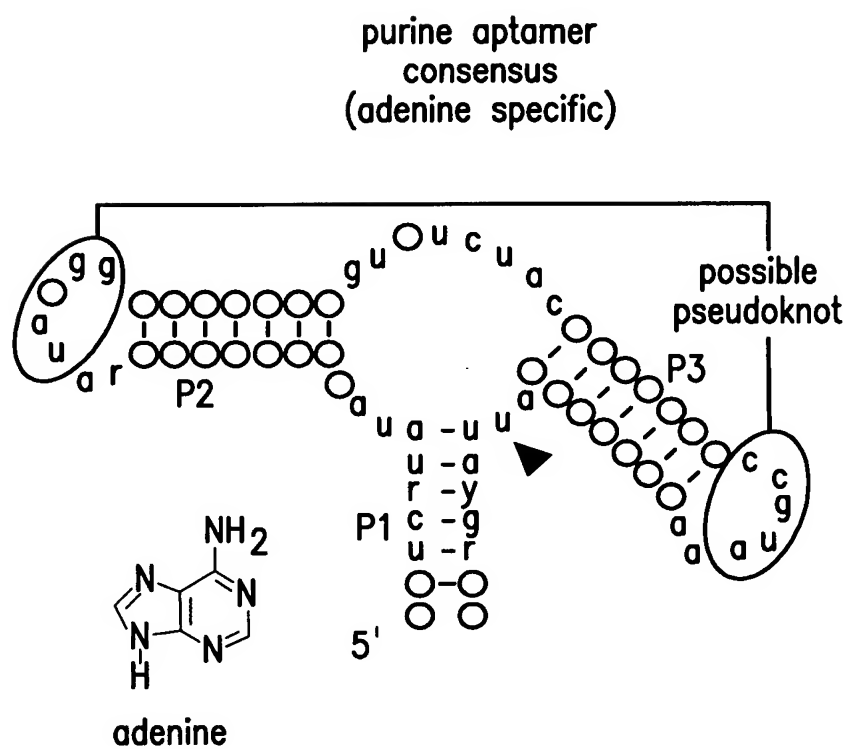


FIG. 11F

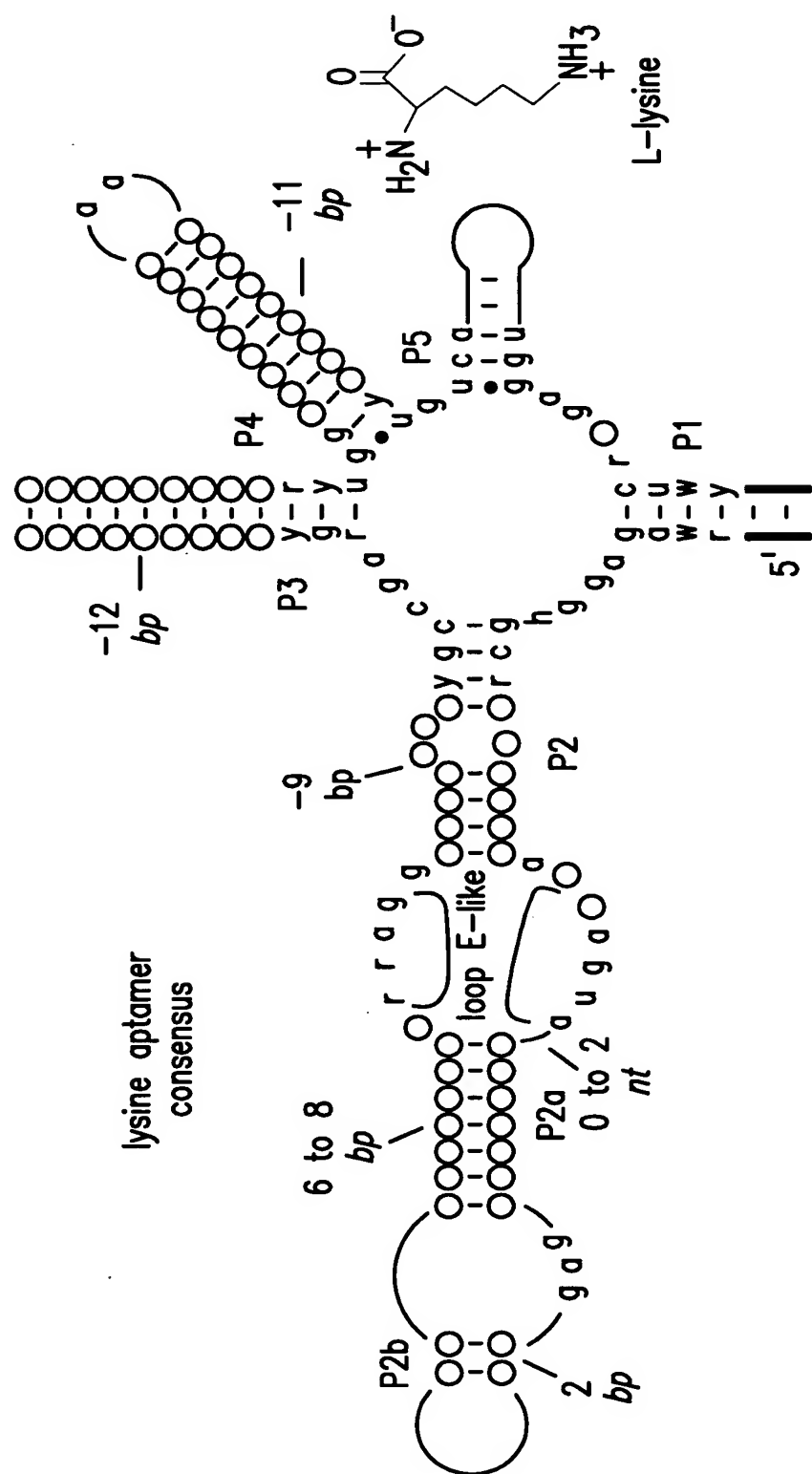


FIG.11G



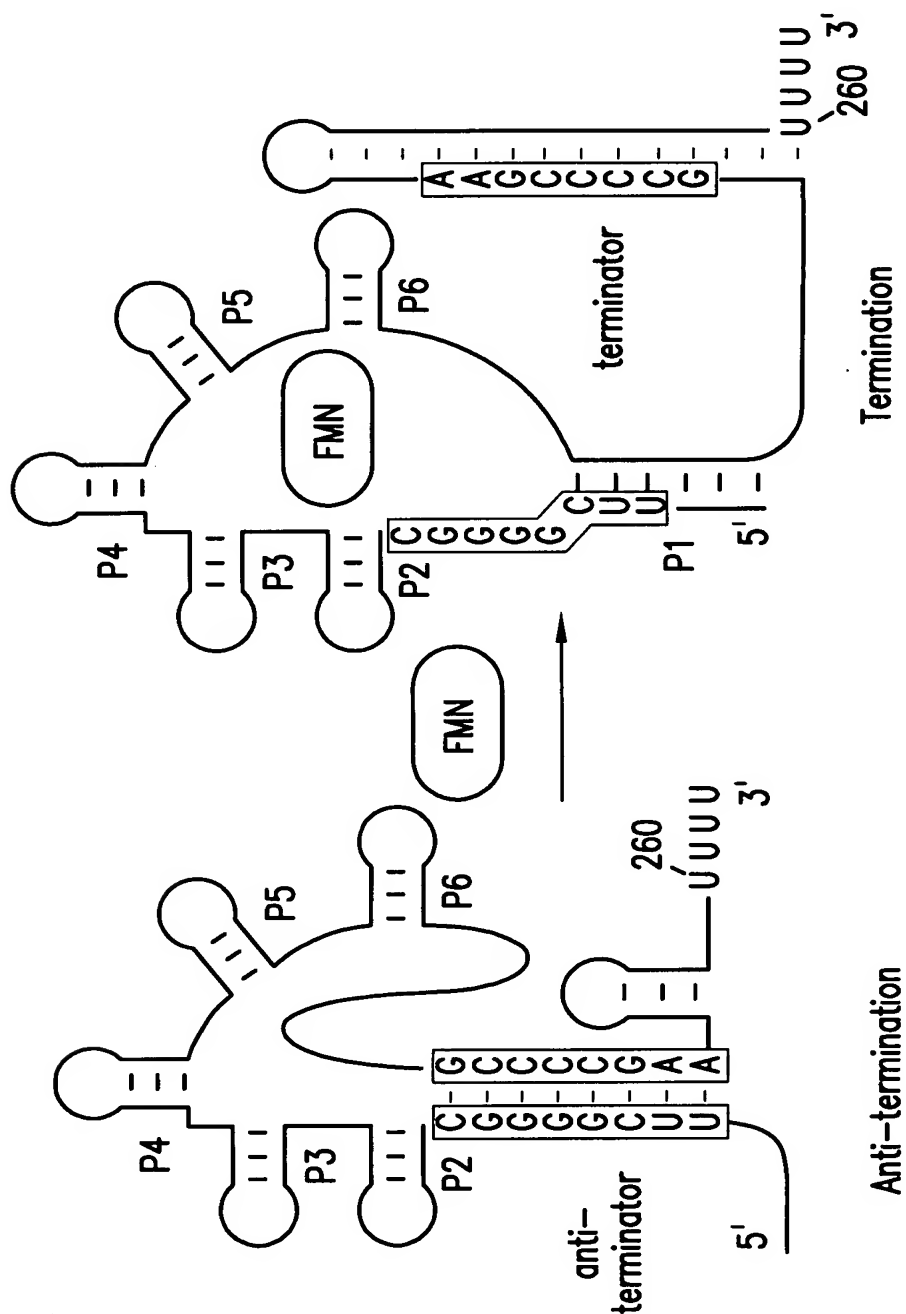
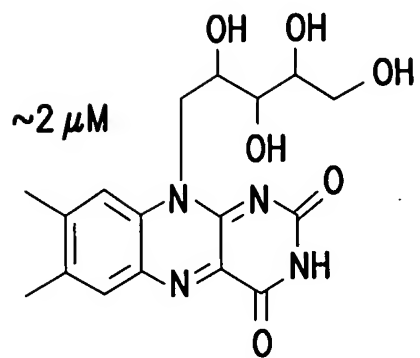
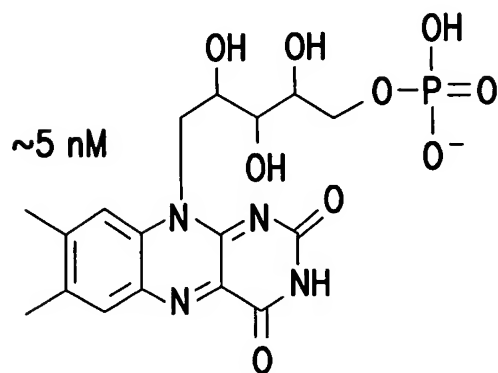


FIG.12B





riboflavin



FMN

FIG. 12C

[illegible][illegible]

**FIG. 13B**

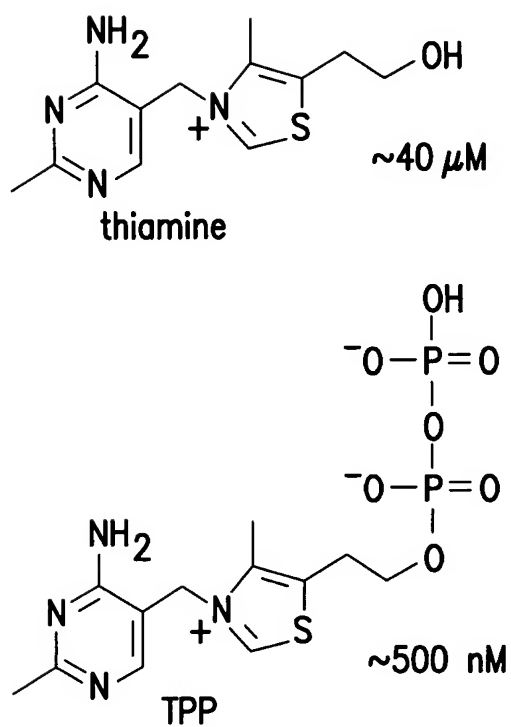


FIG. 13C

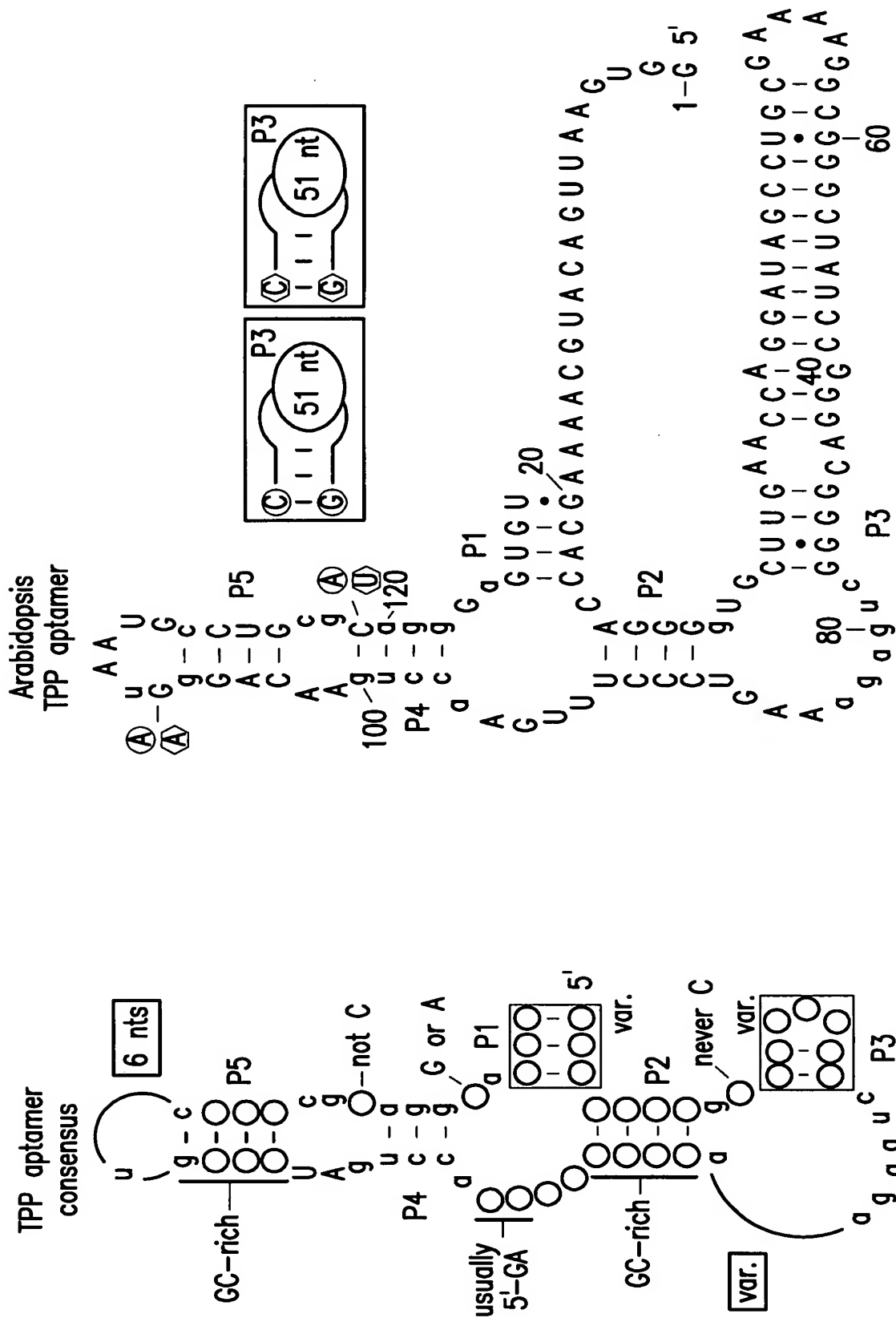
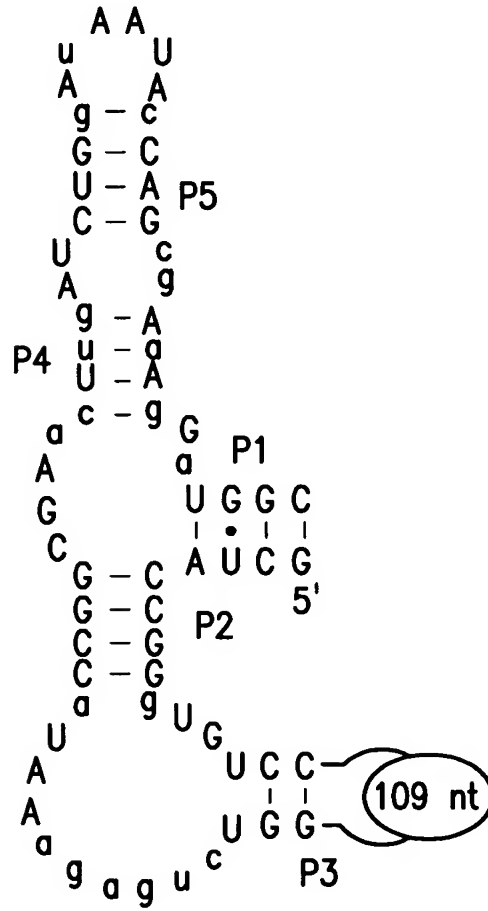


FIG.14B

FIG.14A

## TPP aptamer



**FIG. 14C**

ID	Position	Accession	Sequence Name	Gene	Location
Eco1	-	2183373	NC_000913.1 Escherichia coli K12 complete genome	thiM operon	5'UTR
Eco2	-	4193775	NC_000913.1 Escherichia coli K12 complete genome	thiC operon	5'UTR
Cac	-	3156135	NC_003030.1 Clostridium acetobutylicum ATCC824 complete genome	thiC	5'UTR
Ncr	+	664	AY007661.1 Neurospora crassa thiamine biosynthesis protein nmt-1 gene	nmt-1	5'UTR
Aor	+	622	AF217503.1 Aspergillus oryzae putative thiazole synthase (thiA) gene	thiA [thi4]	5'UTR Intron
Fox	+	2156	AB033416.1 Fusarium oxysporum sti35 gene for stress-responsive gene product	sti35 [thi4]	5'UTR Intron
Fso	+	461	M33642.1 Fusarium solani ST135 protein gene	sti35 [thi4]	5'UTR Intron
Ath	-	78516	AC005496.3 Arabidopsis thaliana chromosome 2 clone T27A16 map mi54	thiamine gene [thiC]	3'UTR
Pse	+	2296	AF264021.1 Poa secunda putative thiamine biosynthesis protein ThiC mRNA	putative thiC	3'UTR
Osa	-	91318	AC084406.7 Oryza sativa chromosome 3 BAC OSJN Ba0067E01 genomic sequence	putative thiC	3'UTR

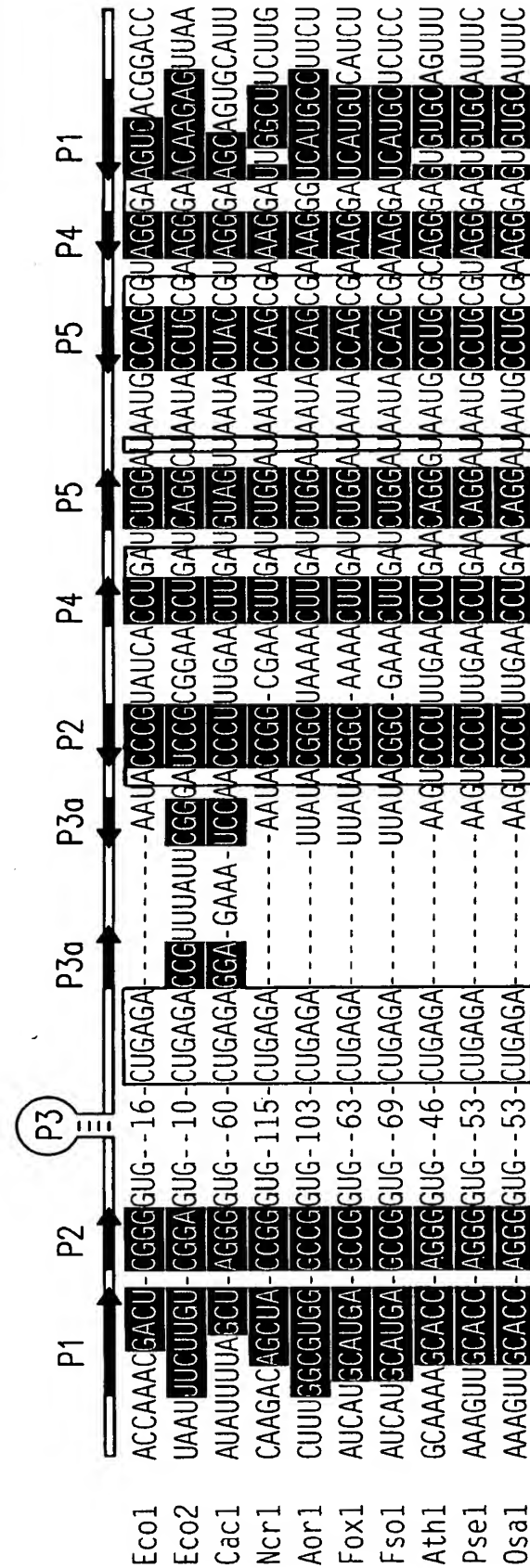


FIG.15

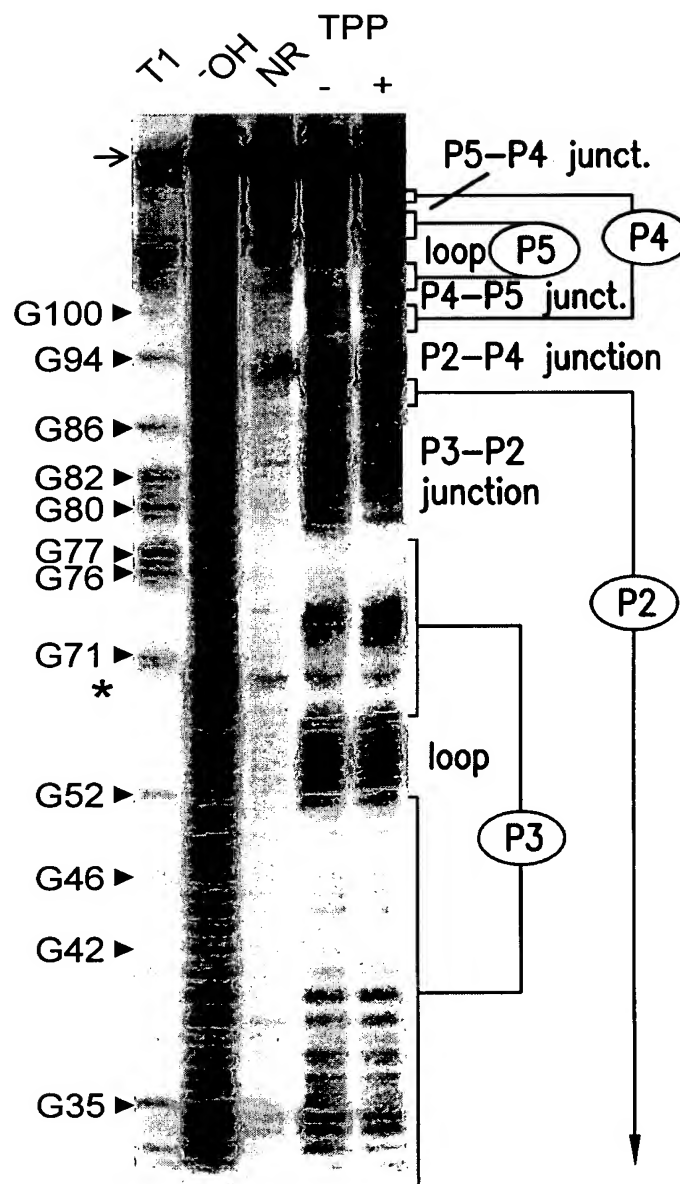


FIG.16A

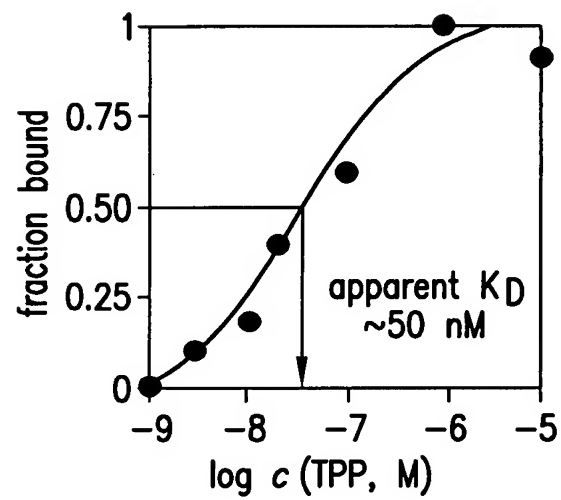


FIG. 16B



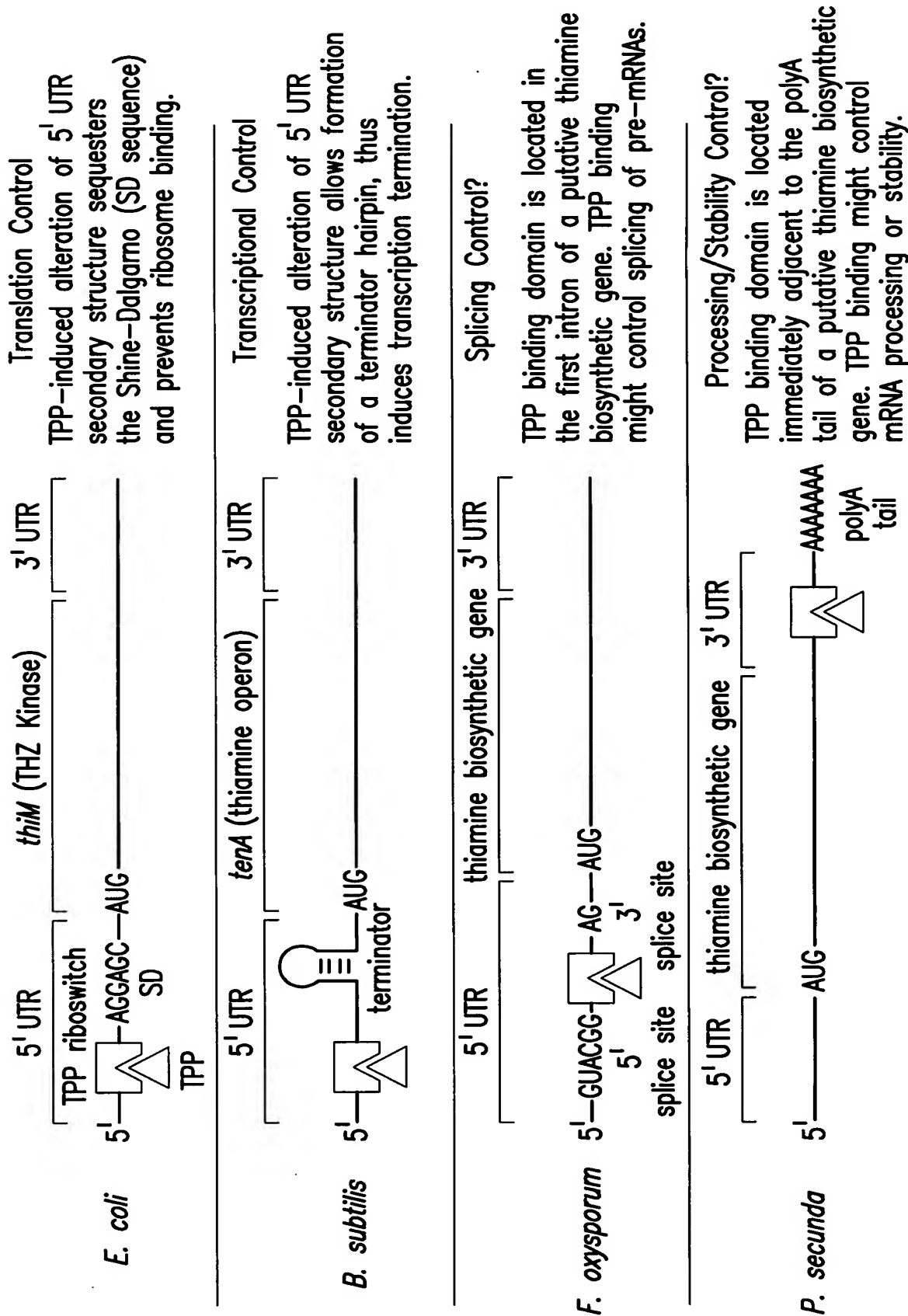
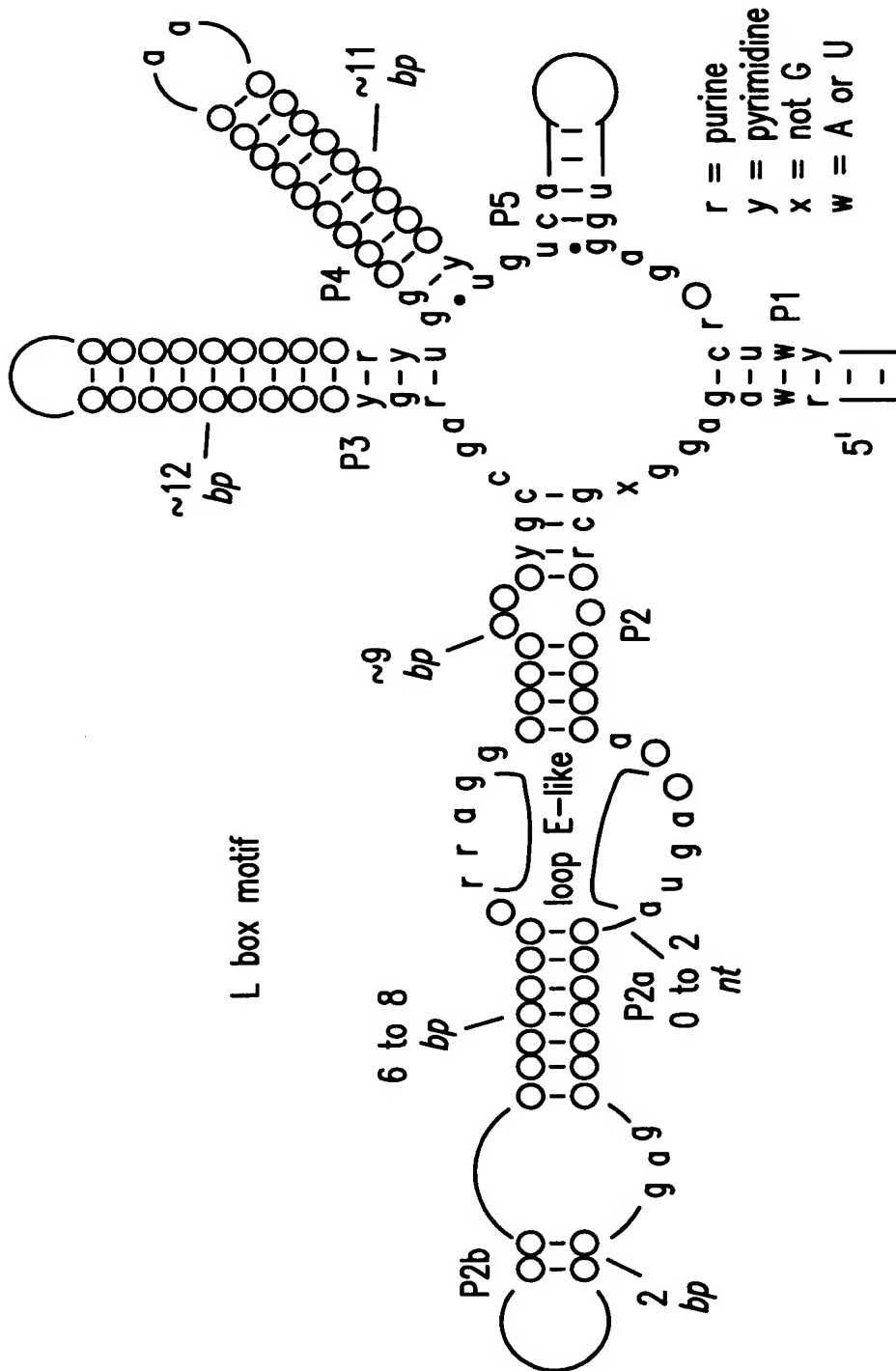


FIG.17

	P1	P2	P2'
1	BA 0845 CGGUGAGGUGagaggUgcAGUUAU--aAG--agua--UCAUUCUG--g--ag--AUAGUC--AUAUGA--AGGAUAGA--GaaaggAAUAGU--Ugcga		
2	BA 1ysA CUCAAGGUGagaggCCgcGAUAGG--aAAGagua--AGCUAUGG--g--ag--UUAUUG--AA--GGUU--GaaaggGACUUA--Ugcga		
3	BA 1ysP CGAUGAGGUGagaggUgcGACUUAU--aAG--agua--AAAGCGAC--g--agAACGAGAA--GUCUAAGA--UCCGUUU--GaaaggAAAGU--Ugcga		
4	BH dapa AGUGAGGAGUagaggUgcAAAAACC--aAG--agua--CACAAU--Gg--ag--GAGAUGAGA--UCCGUUGAGAAUUG--GaaaggGGAA--UUUgcga		
5	BH 1ysC AGUGAGGUGagaggUgcGAAACC--aAG--aguaC--ACAGUC--UCAG--ag--AAUGAGAAUCCUUC--GACUUUGGaaaggGGGA--UUCgcca		
6	BH nhac AGAUGCGGUGagaggUgcGGGUUU--aAG--aguaA--GCGCUUG--g--agGALGACAA--CGAGGA--UAAGCGG--CGaaaggAAA--UUCgcca		
7*	BS 1ysC GGUGAGGUGagaggUgcGAGCUUC--aAG--aguaU--GCCUUU--Gg--ag--AAAGAUGGA--UUCUGUGAA--AAAGGC--UGaaaggGGAGCG--Ucgcca		
8	CA 1ysA ACCUUUUGUagaggUgcUUAAGUCAG--aguaA--CGUUUG--g--ag--UUGGCA--AACUUGA--UGAACGG--UaaaggGGCUUU--Agcca		
9	CP 1ysA GACCAAGGUGagaggUgcGUAAU--aAG--agua--GUCUAU--Aglag--CUGACA--AG--9--UAUGU--GaaaggGAU--AUGgcca		
10	CP 1ysP AACUGAGUagaggUgcGALCAU--aAU--agua--UUUUGG--Ag--ag--GUAAGCA--AUGAA--GCAAG--UGaaaggAUGA--AUGgcca		
11	CP nhac AAAGAGGUGagaggUgcGAGAUUC--aAG--agua--CUAAAU--Gg--ag--UUAAGU--ACGUAGAGUUUAG--GaaaggGAUUA--Cgcca		
12	EC 1ysC CAGGCCAGagaggUgcGUUGCCC--a--aguaAGGUGUG--g--ag--GAGCCAG--UCCUGUGA--UAACCC--UgGGUGCAUCgcca		
13	HI nhac UACAAAGUagaggUgcAAUUAU--aUA--agua--UUUUUG--Ag--ag--UGSAUA--CGAGAA--GAAAAA--GaaaggAAUAGU--Ugcga		
14	OI dapa GUUUUGGUGagaggUgcGGAGAC--aUC--agua--UUAAGC--Ggag--GGAAGAG--CGUAUG--GGAAG--GaaaggGGAA--UcUgcca		
15	OI nhac UCGUGGUGagaggUgcAUACAAC--aUU--agua--AUCCAG--Aag--agGALGACAA--CGALCAUA--GUUGU--GGaaaggGUUU--Ugcga		
16	PM nhac UACUUGUGagaggUgcGALCACU--aUA--agua--UUUUUCU--g--ag--UGSAUA--CGAAG--GAAAAAG--GaaaggAGUGAC--Cgcca		
17	SA 1ysC AUUUUUGUagaggUgcAUCNAUC--aUG--agua--AGUUUA--g--aU--UACUGUUGC--UAACAG--UGAAUU--GaaaggGUEC--GAUgcca		
18	SA 1ysP AUUGAGUagaggUgcAUGUUA--aUU--agua--ACUUGU--Cagag--UAUUUGG--UA--10--ACAAGU--GaaaggUAAG--AUgcca		
19	SE 1ysC AGAUUUGUagaggUgcAUCNAUC--aUG--agua--AACUUUA--g--aU--UAUUCUUGCUACAUAUUAAGAU--AaaaggUGA--GAUgcca		
20	SE 1ysP AUUGAGUagaggUgcAUUAUA--aUG--aCua--ACUUAU--Cagag--UUGUUGG--GA--10--AUAGU--GaaaggUAUAU--gcca		
21	SF 1ysC CAGGCCAGagaggUgcGUUGCCC--a--aguaAGGUGUG--g--ag--GAGCCAG--UCCUGUGA--UAACCC--UGaaggGGUGCAUCgcca		
22	SO 1ysC AGGAACAGagaggUgcGUUAACU--a--Gua--GUCAUUA--GAGg--agCAAAACUCCAGCA--UGAUUGU--GAGgaga--UAAGCgcca		
23	SO nhac CCUUUAGUagaggUgcGUUGCCU--aUG--aCua--CUUGUGG--g--ag--GGUGAUG--CGGAGA--UGUAAG--GaaaggAGU--CAGGgcca		
24	TM asd UGACCGAGagaggUgcGCCCGAG--aUG--agua--GGUGUCCC--7--g--ag--GAA--UCC--GGGACGGCU--GaaaggGAGGG--Cgcca		
25	TT 1ysA AGGUGAGGUGagaggUgcGGGUCAUGaAG--agua--ACAUGC--Ag--ag--GUGUA--AG--10--GGUGUG--GaaaggGGUG--CCGgcca		
26	TT psf CGCAUAAUagaggUgcUCCCAAGCaU--gualUUUGCCAG--10--gagAACCUCCAAUA--CUCCUG--AAGaaaggUUUGG--Ugcga		
27	VC 1ysC UCUAGCAGagaggUgcACUGCCC--aGGCag--aUGUUUGG--g--agCCUCAACUCCAA--UACAGAUAUCCagGGAGUAGUgcca		
28	VC nhac UUUCCCGUagaggUgcGGUUAOC--aAA--agua--UCCACAGU--g--Gg--GLGAGC--CAUUG--AAUUGUGA--AaaaggGUU--GCCgcca		
29	VC nhac CCUUUAAGUagaggUgcGUGUUC--aUG--aguaC--CCAGUC--gUag--GUAGCCCC--GAUG--AUCACUGG--UUaaaggGU--ACAGGgcca		
30	VV 1ysC UUUUGCAGagaggUgcACUGCCC--aGGCag--aUGUUUGG--g--agCCGCAACUCCAA--CACAGAUAUCCagGGAGUAGUgcca		
31	VV nhac UAUAGAGUagaggUgcAAUGGUA--aAG--agua--ACUAUAU--g--Gg--GUGU--GCCAAUGAAUAUAGU--GaaaggUAU--CCAUUgcca		

FIG. 18A





**FIG. 19A**

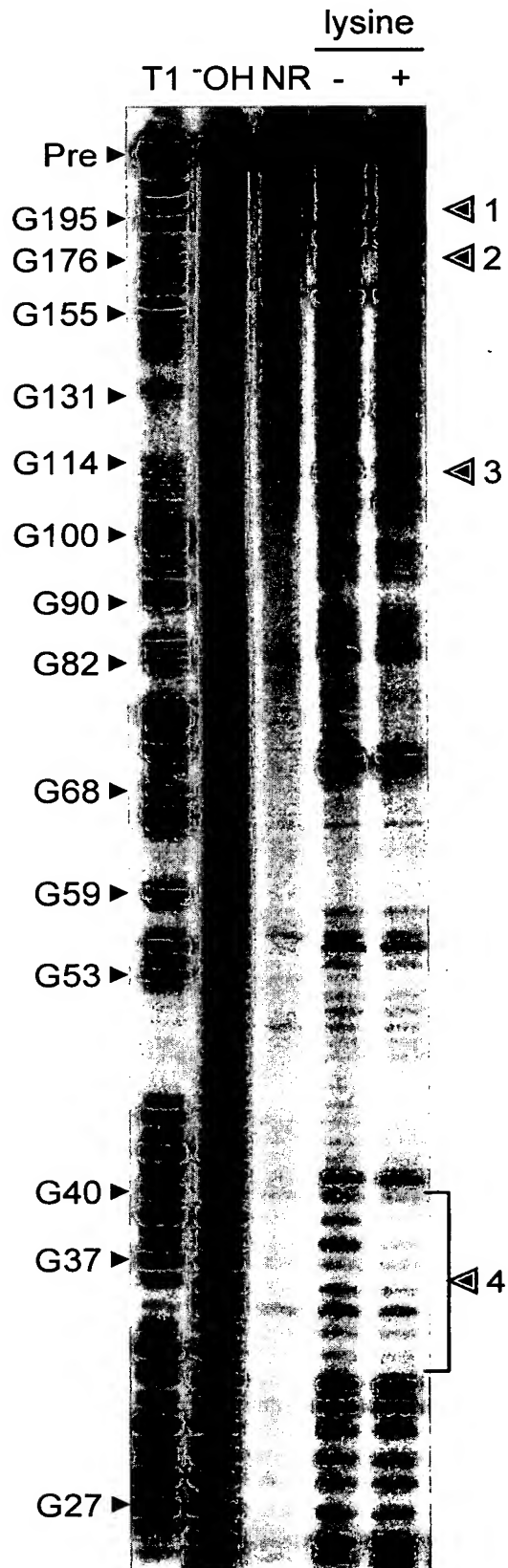


FIG.19B



**FIG. 19C**

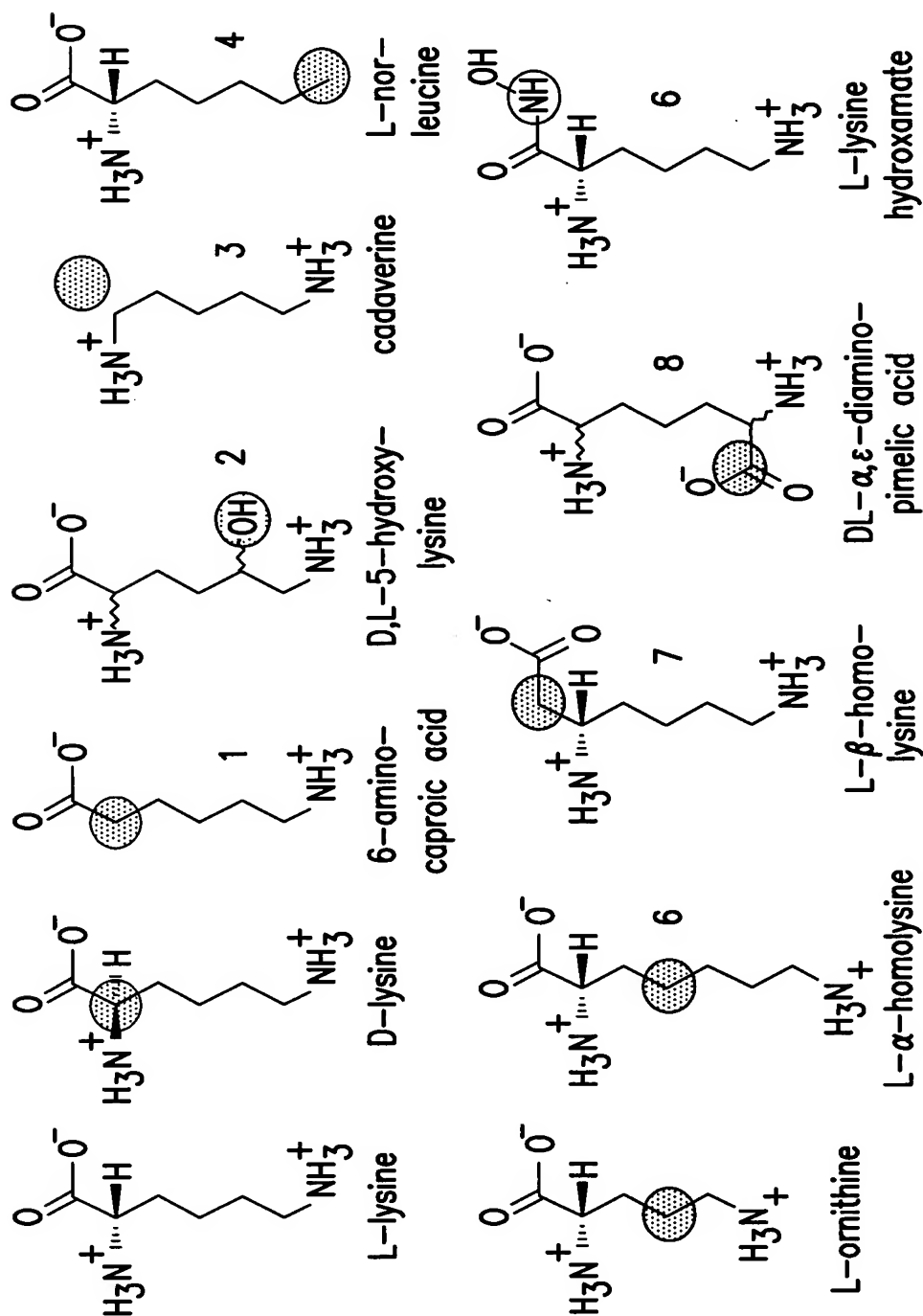


FIG. 20A

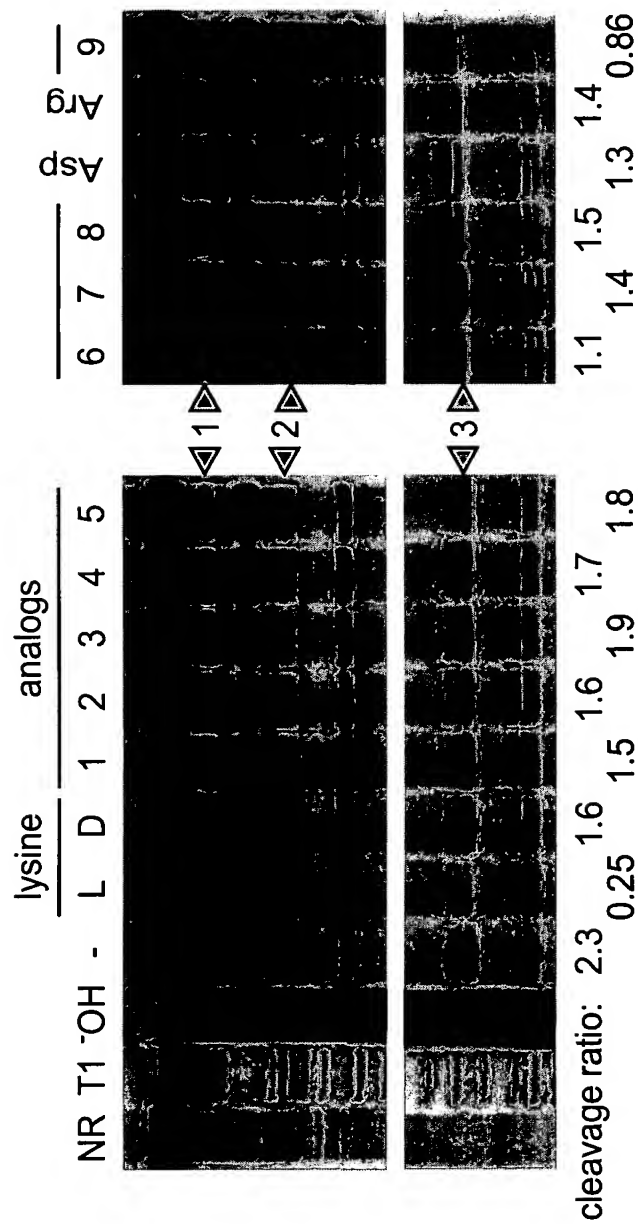


FIG.20B



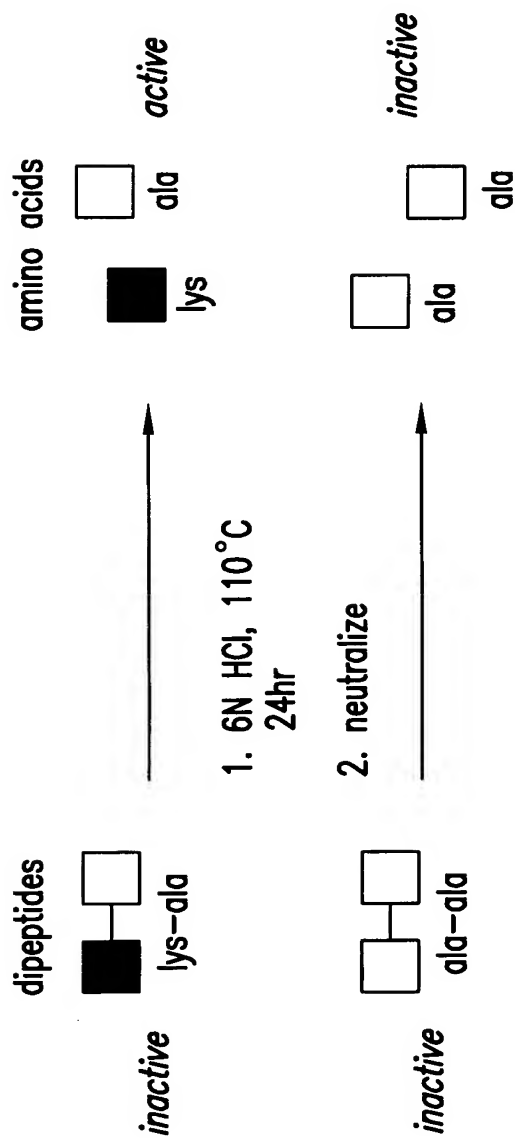


FIG.20C

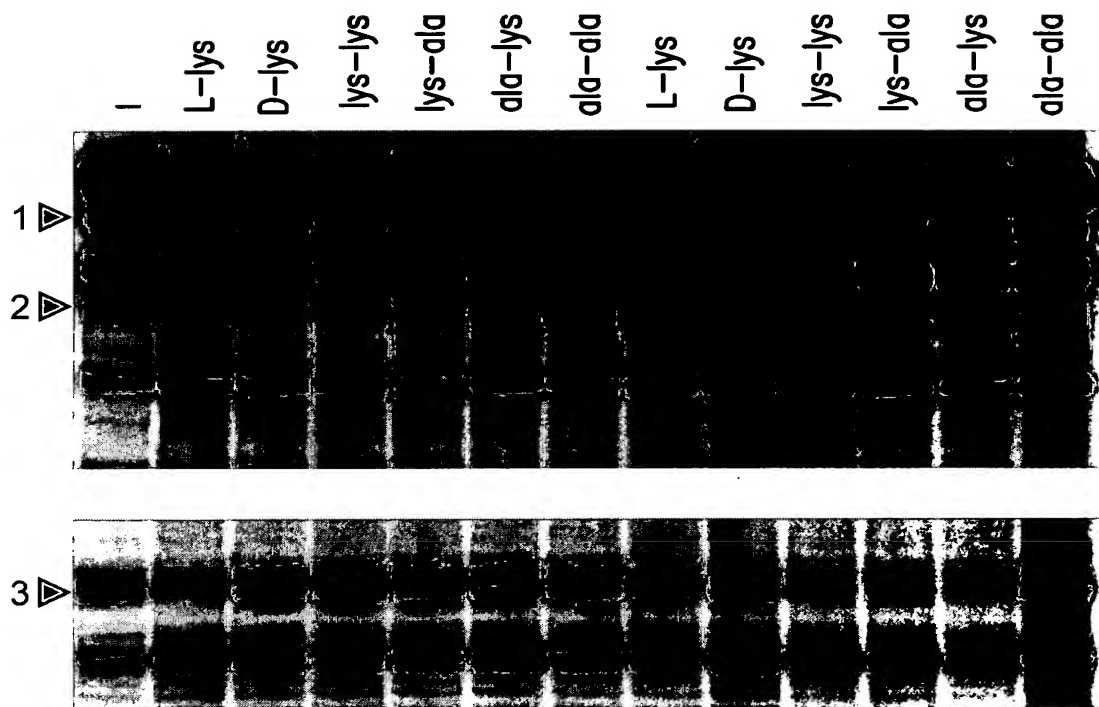


FIG.20D

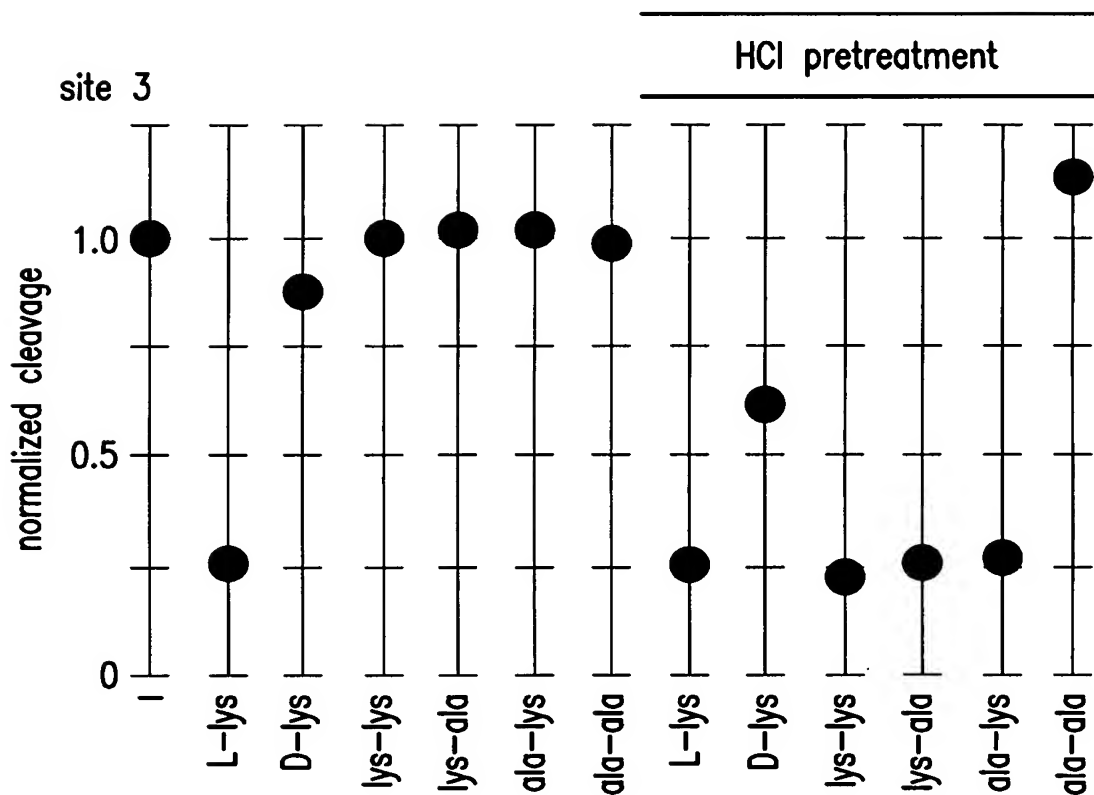


FIG.20E

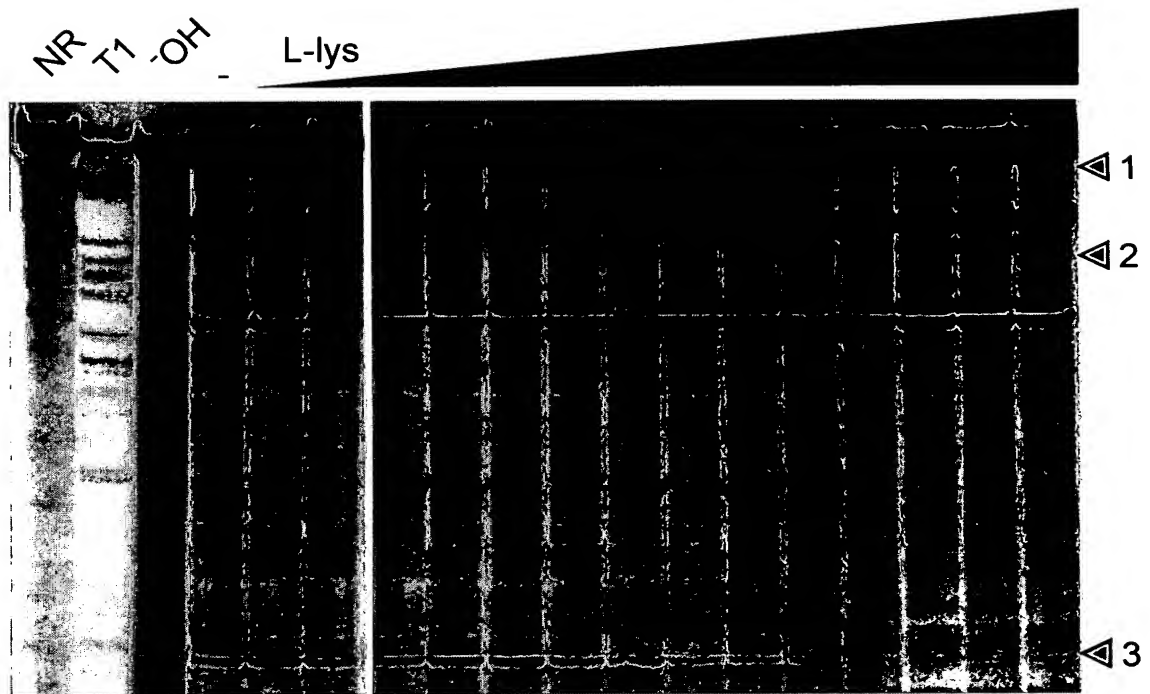


FIG.21A

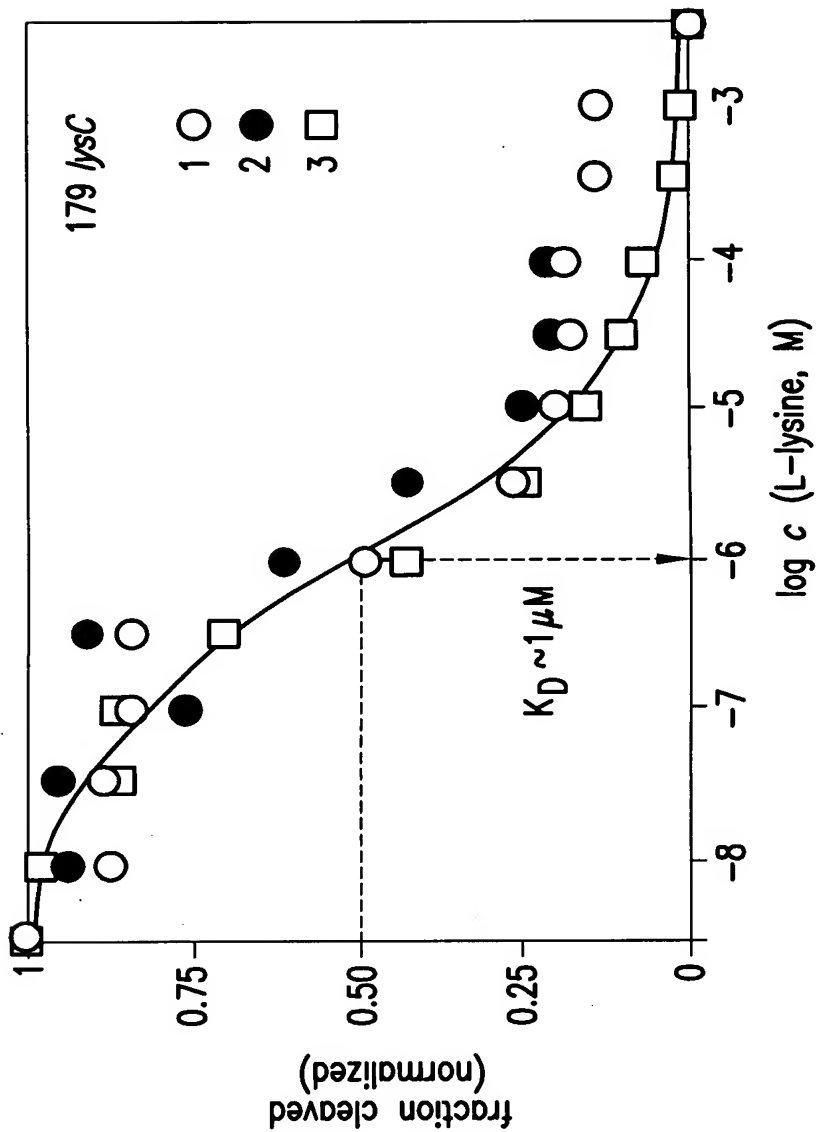


FIG. 21B

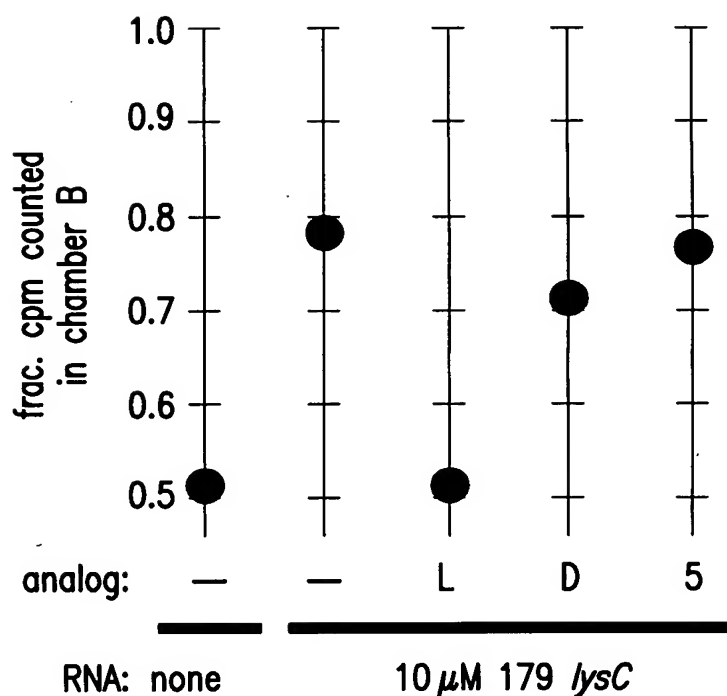


FIG.21C

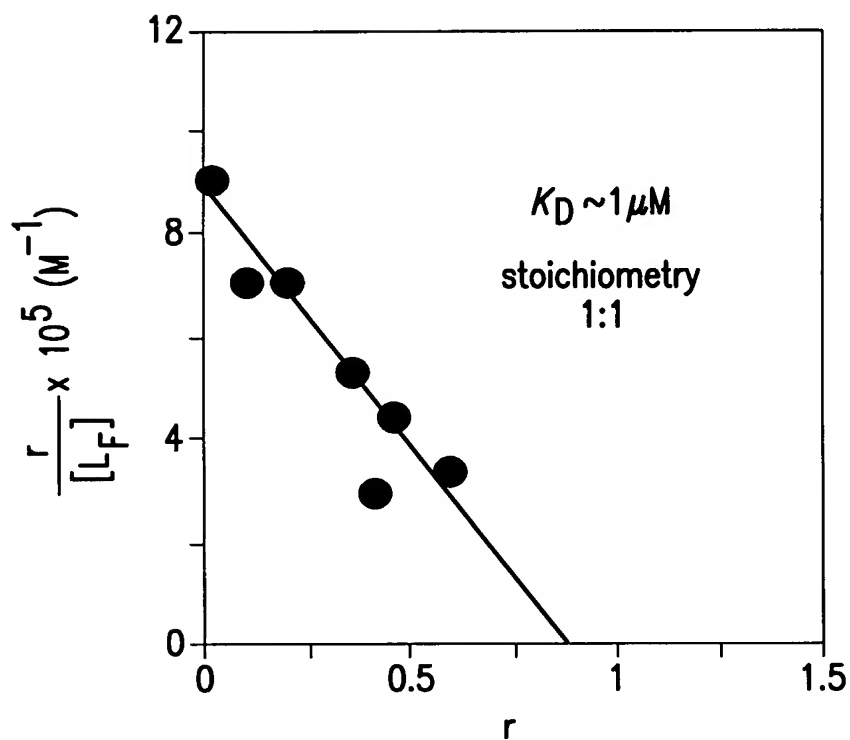
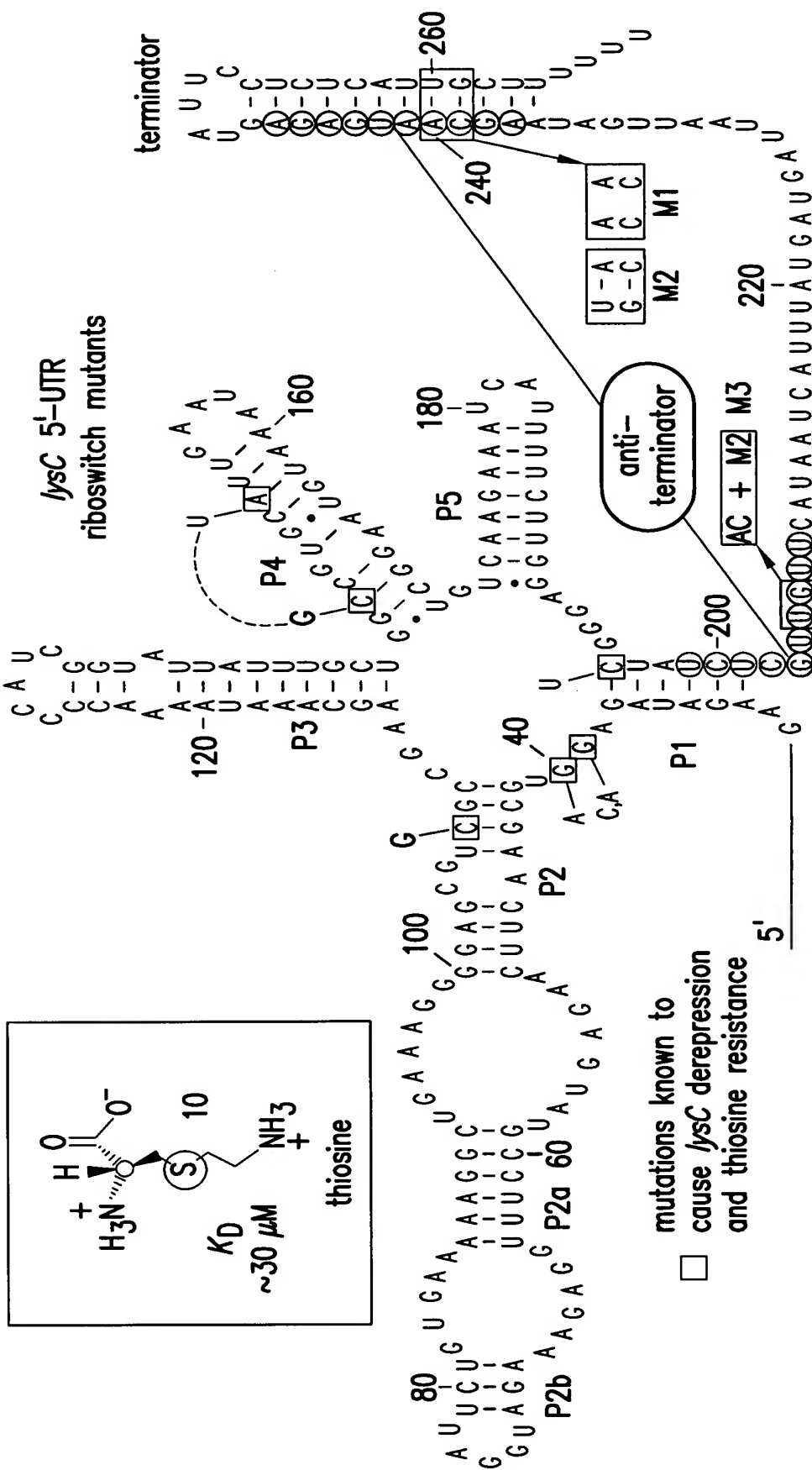


FIG.21D



**FIG. 22A**

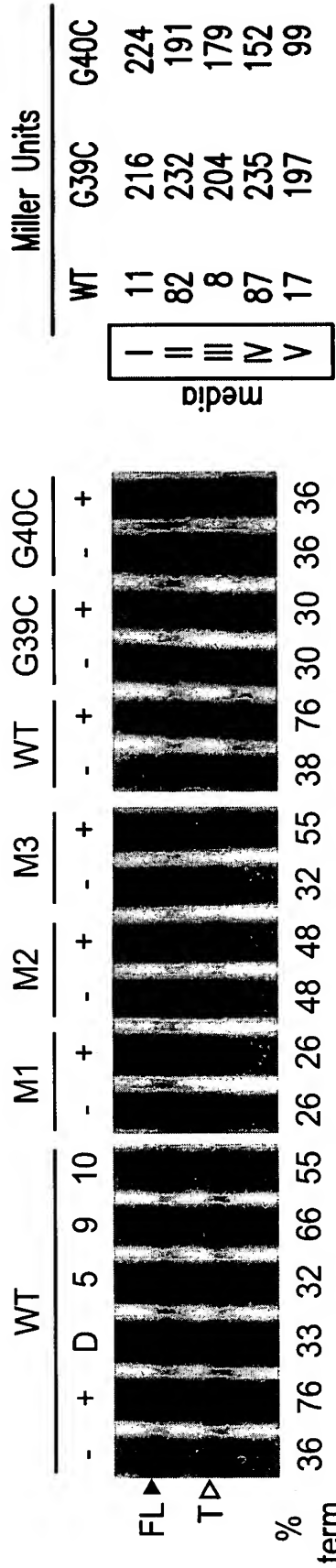
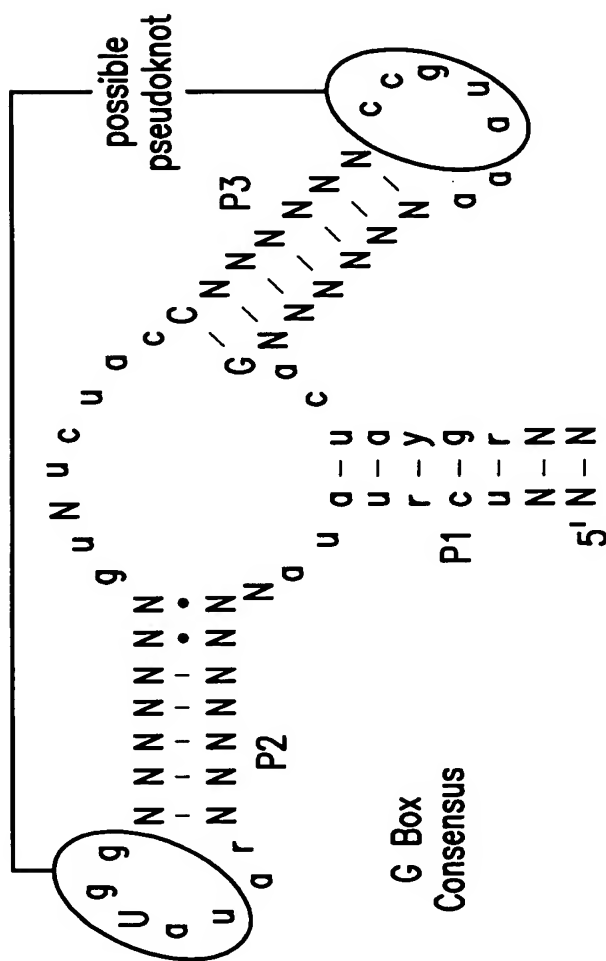


FIG.22B

FIG.22C







**FIG. 24A**



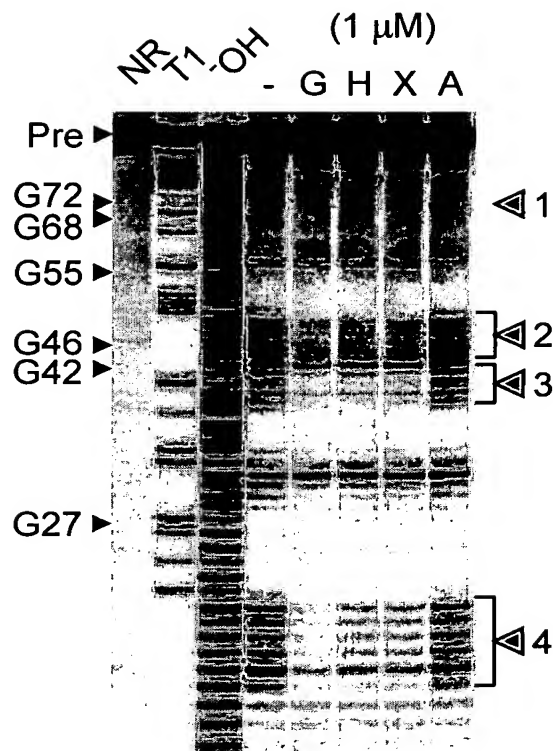


FIG.24C

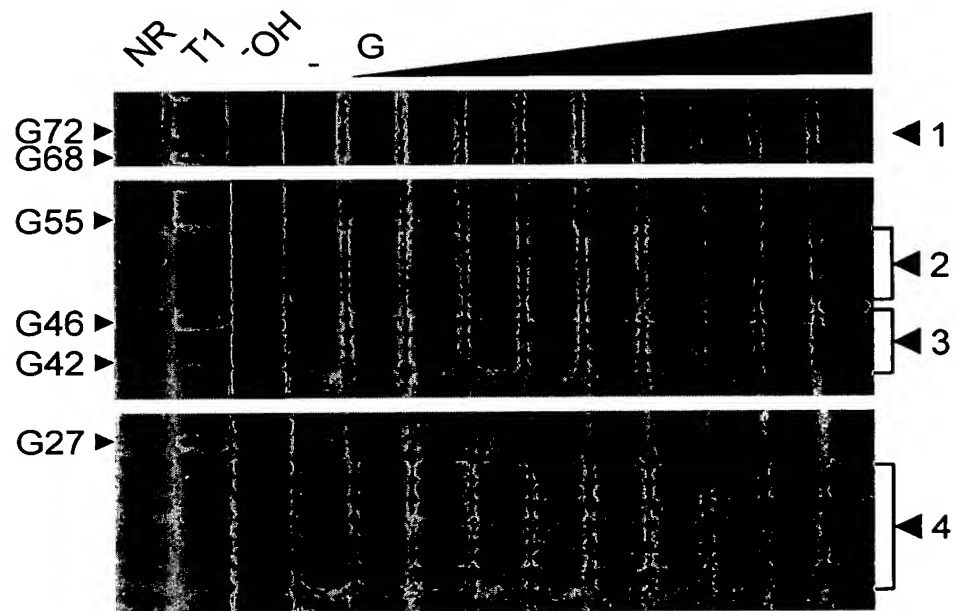


FIG.25A

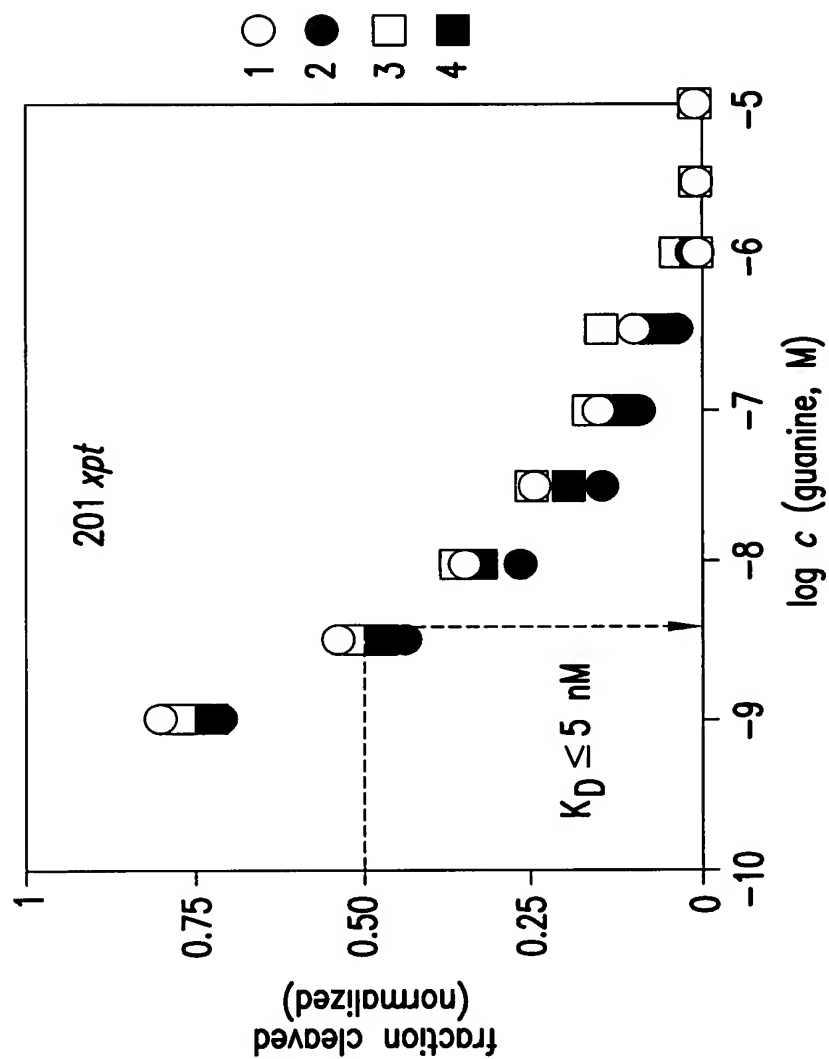


FIG. 25B

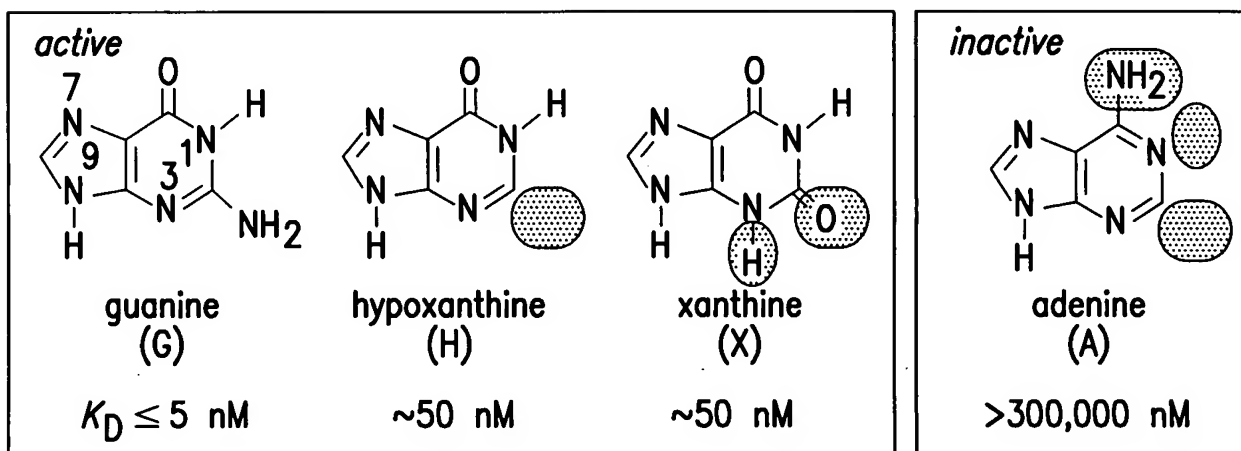


FIG.26A

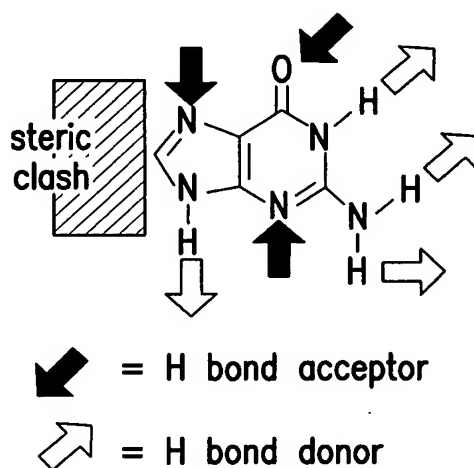


FIG.26C

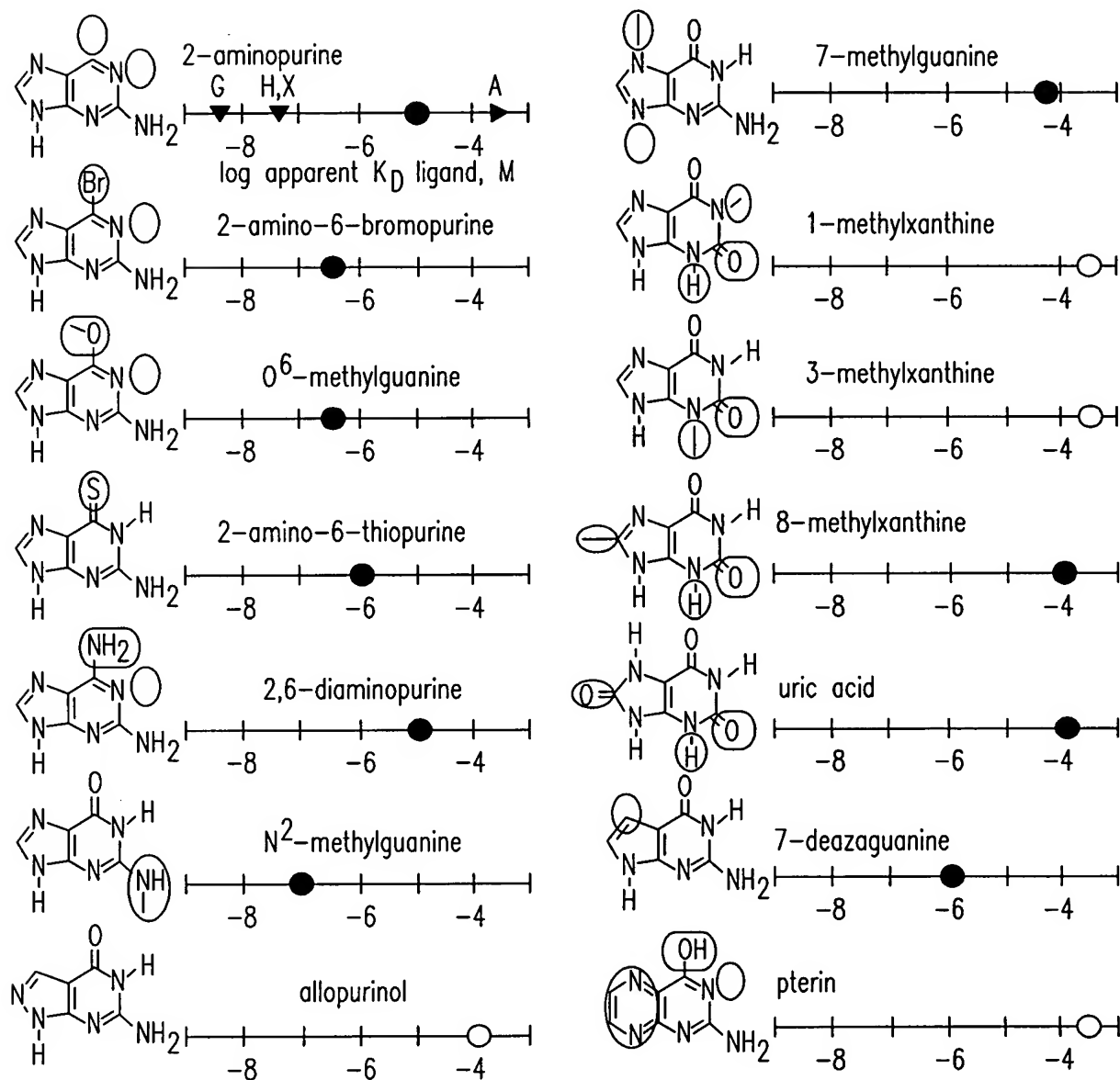


FIG. 26B

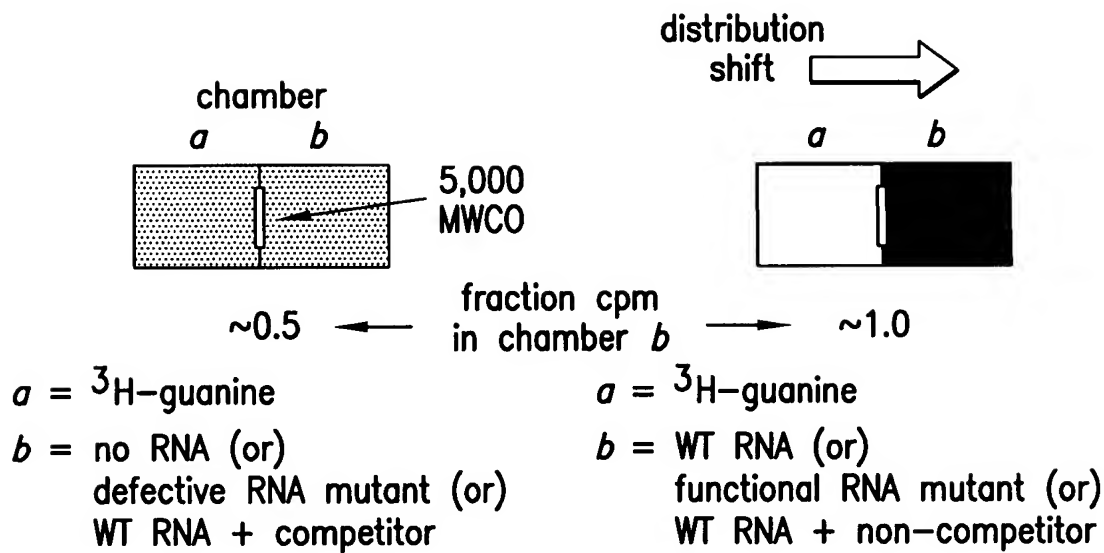


FIG.27A

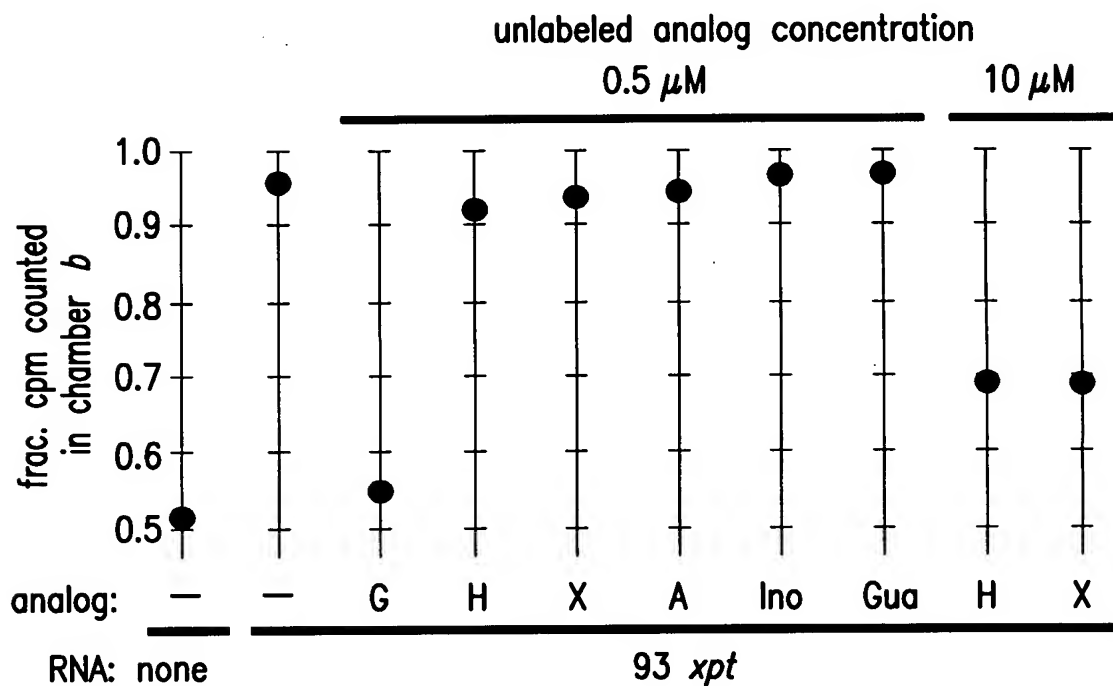


FIG.27B



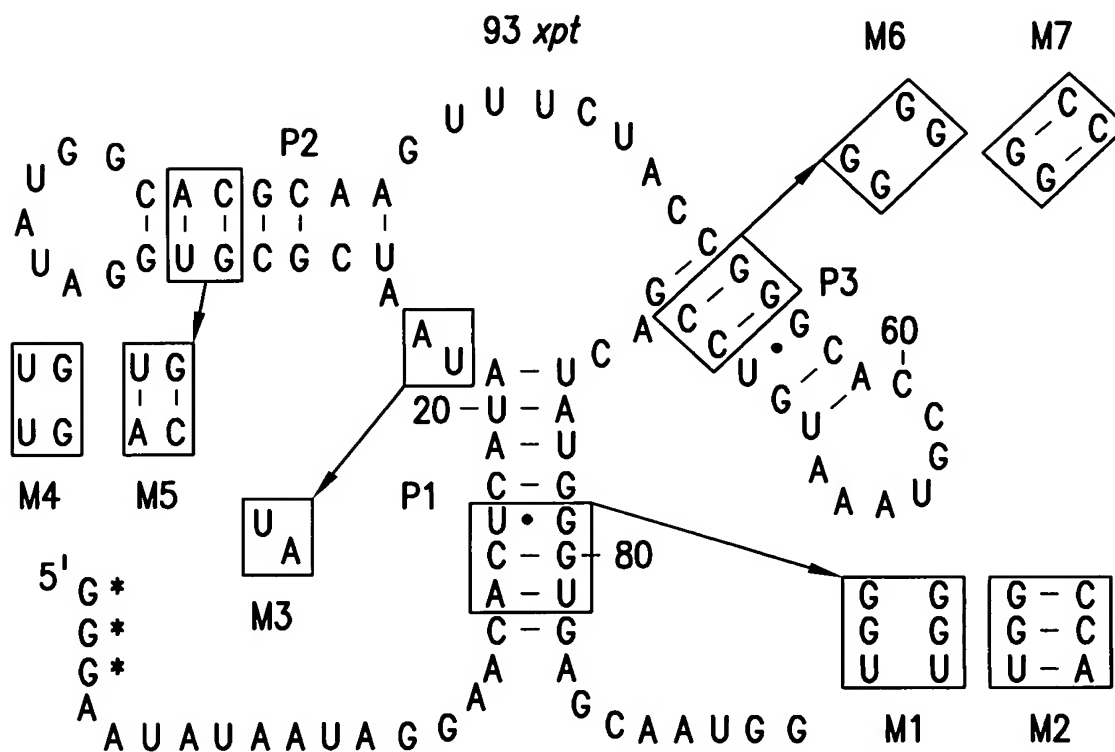


FIG.28A

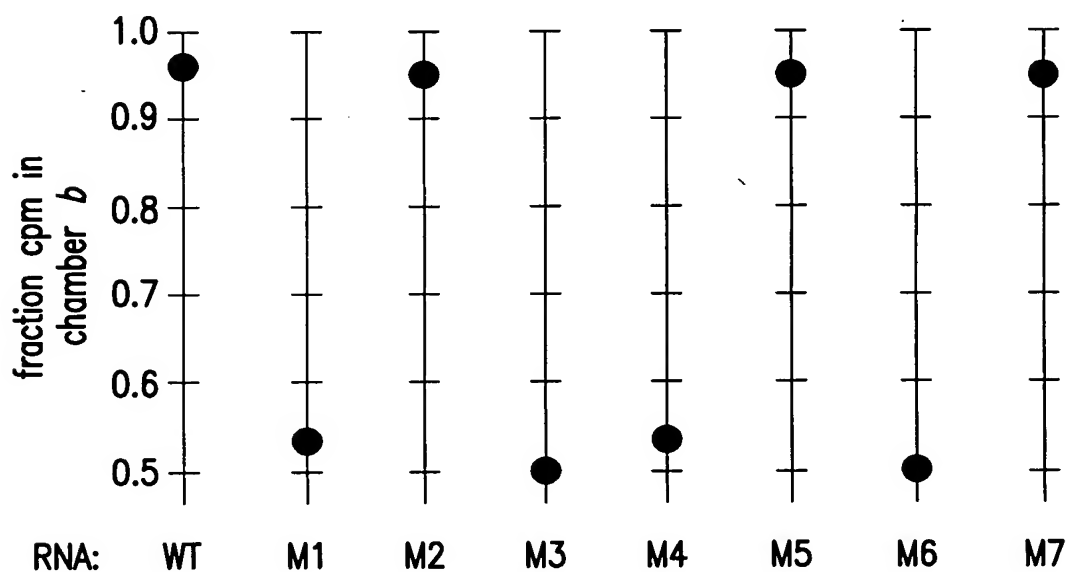


FIG.28B

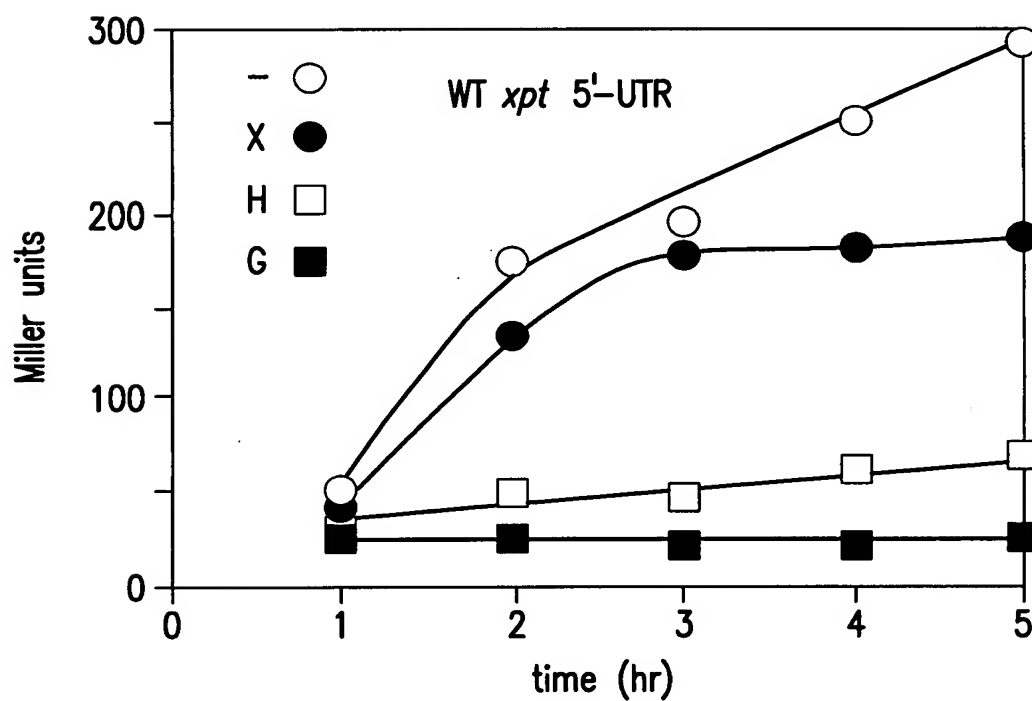


FIG.28C

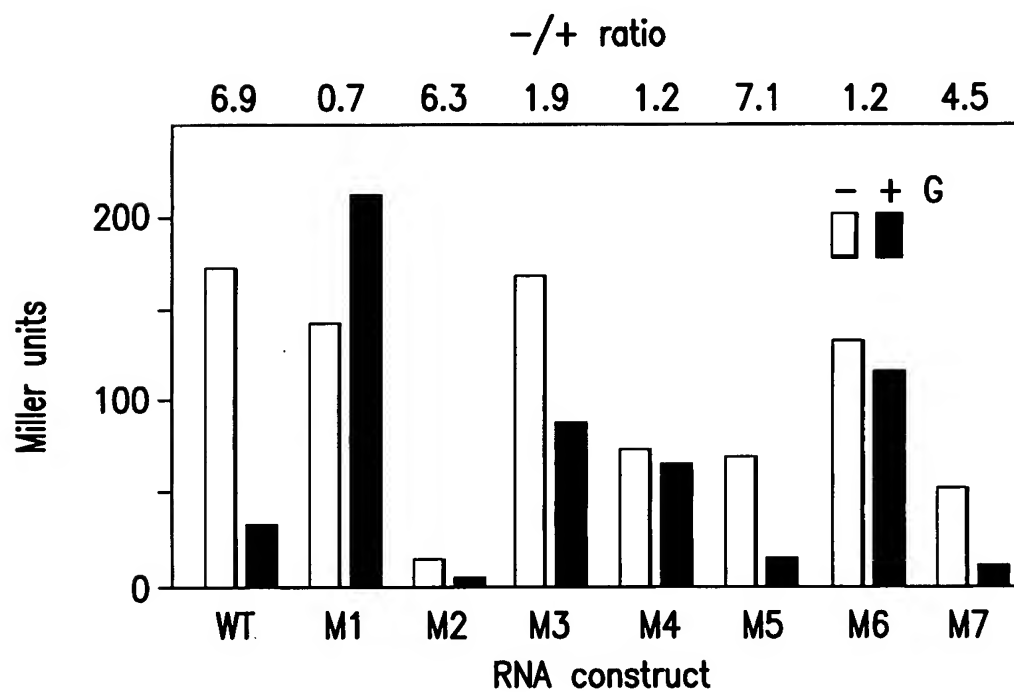


FIG.28D

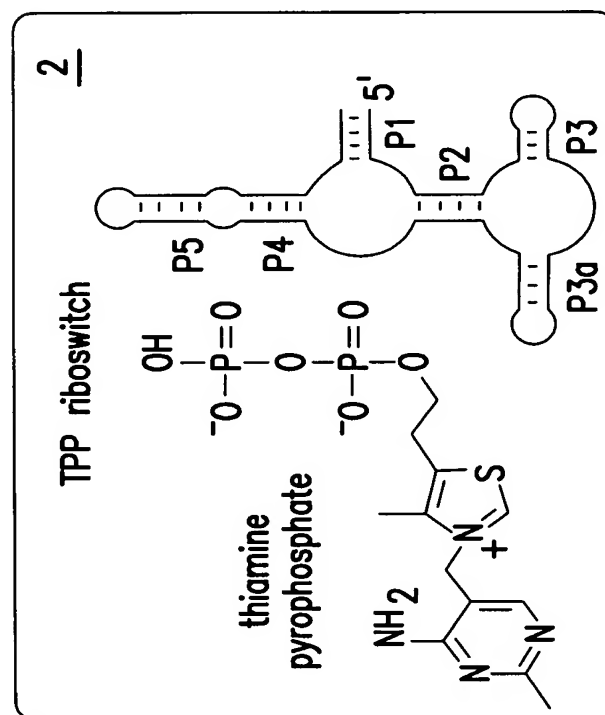
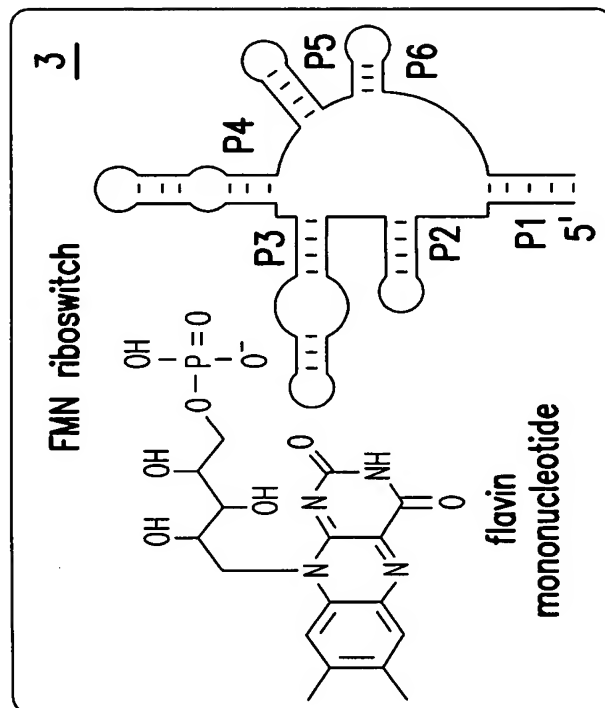
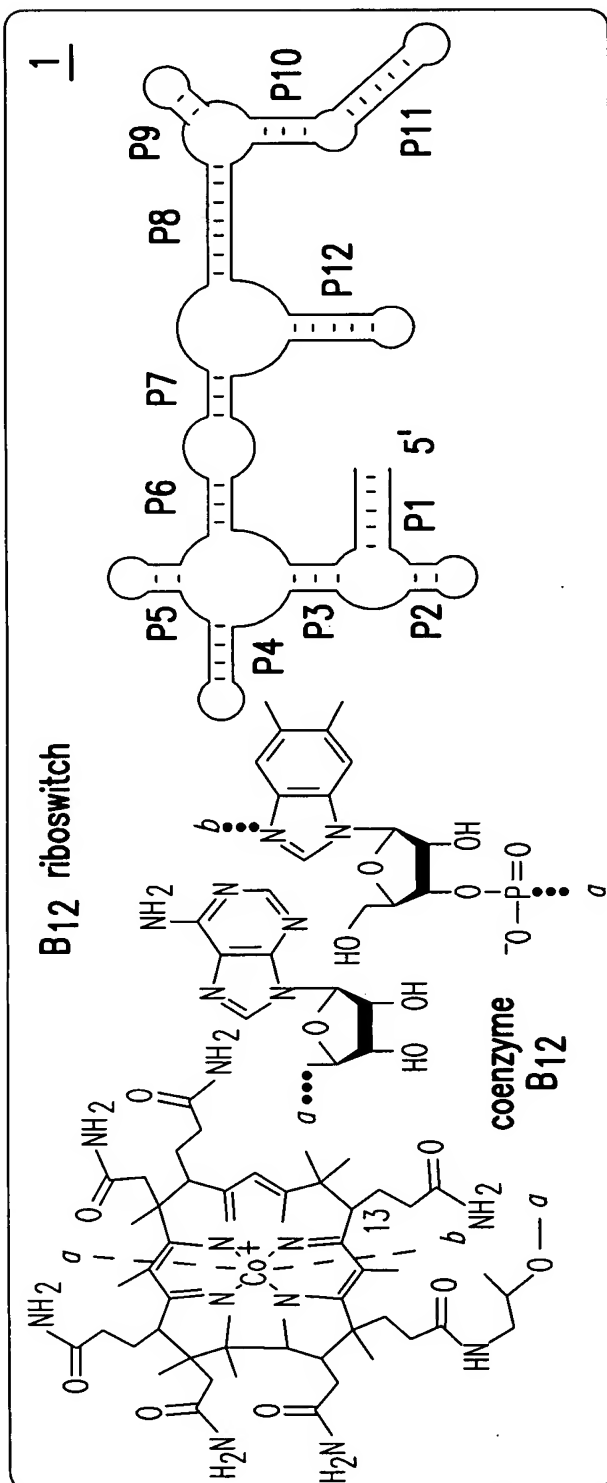


FIG. 29A

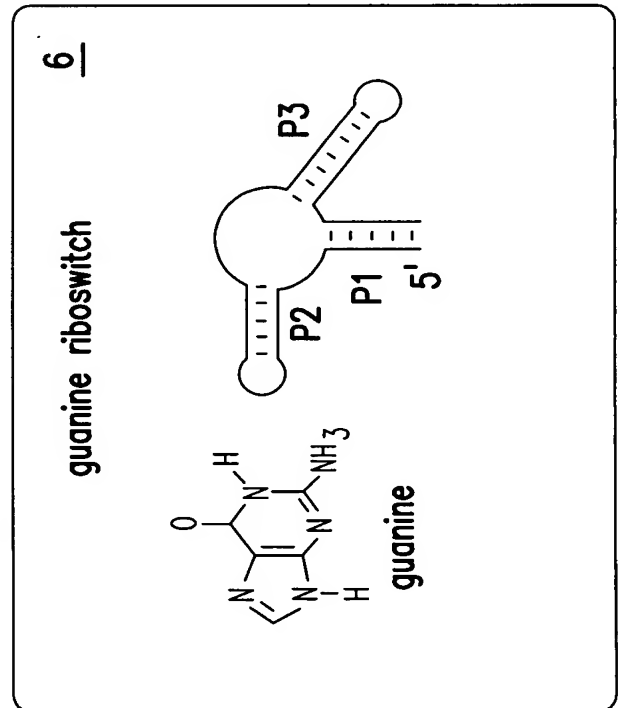
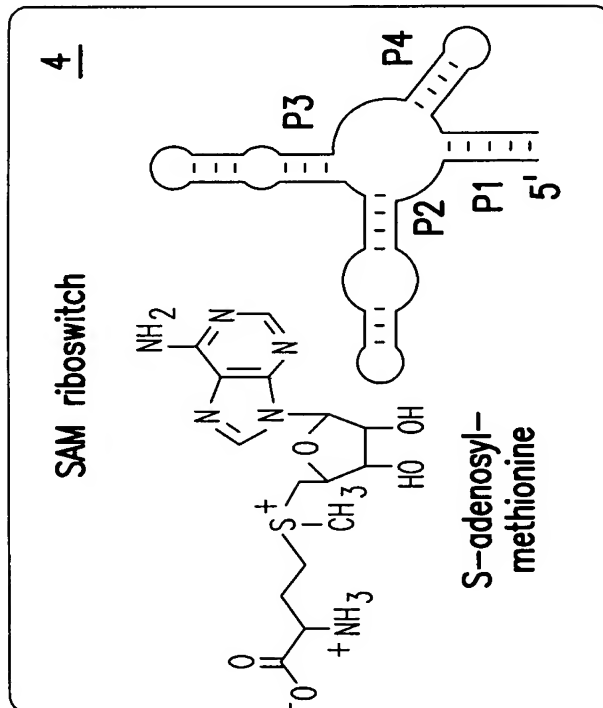
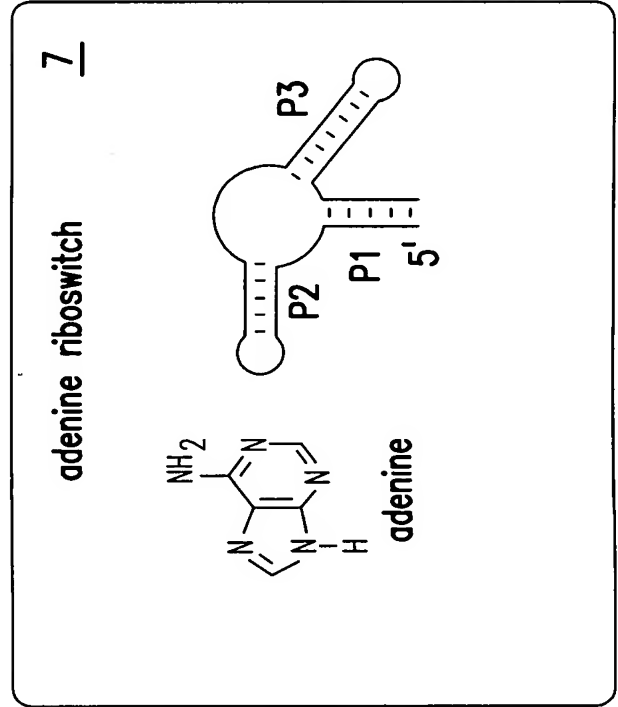
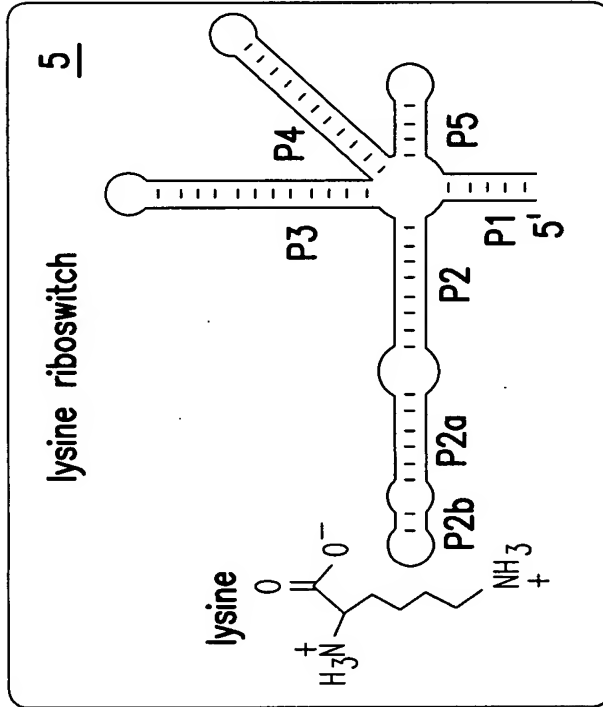


FIG. 29A-1

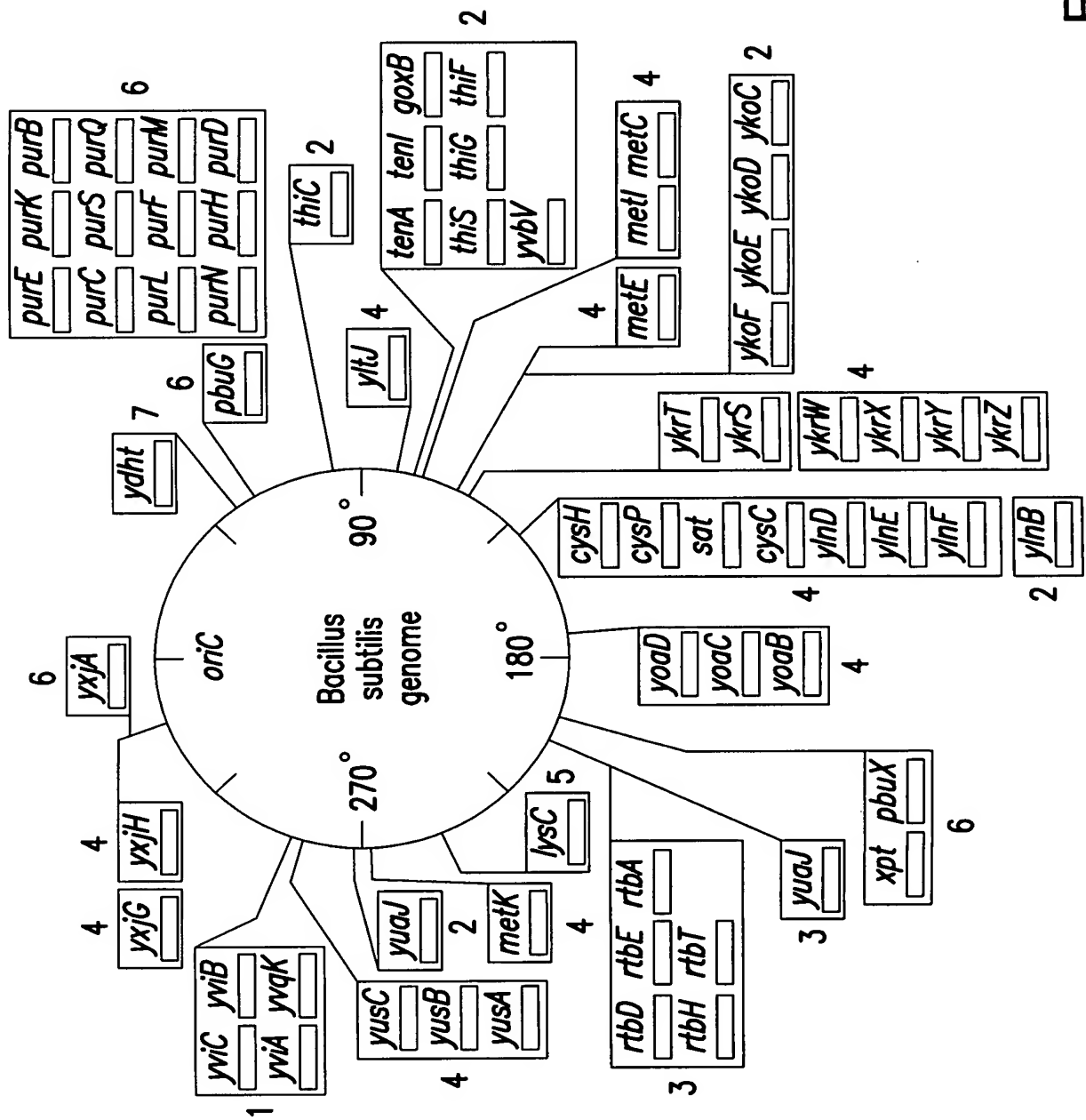


FIG.29B

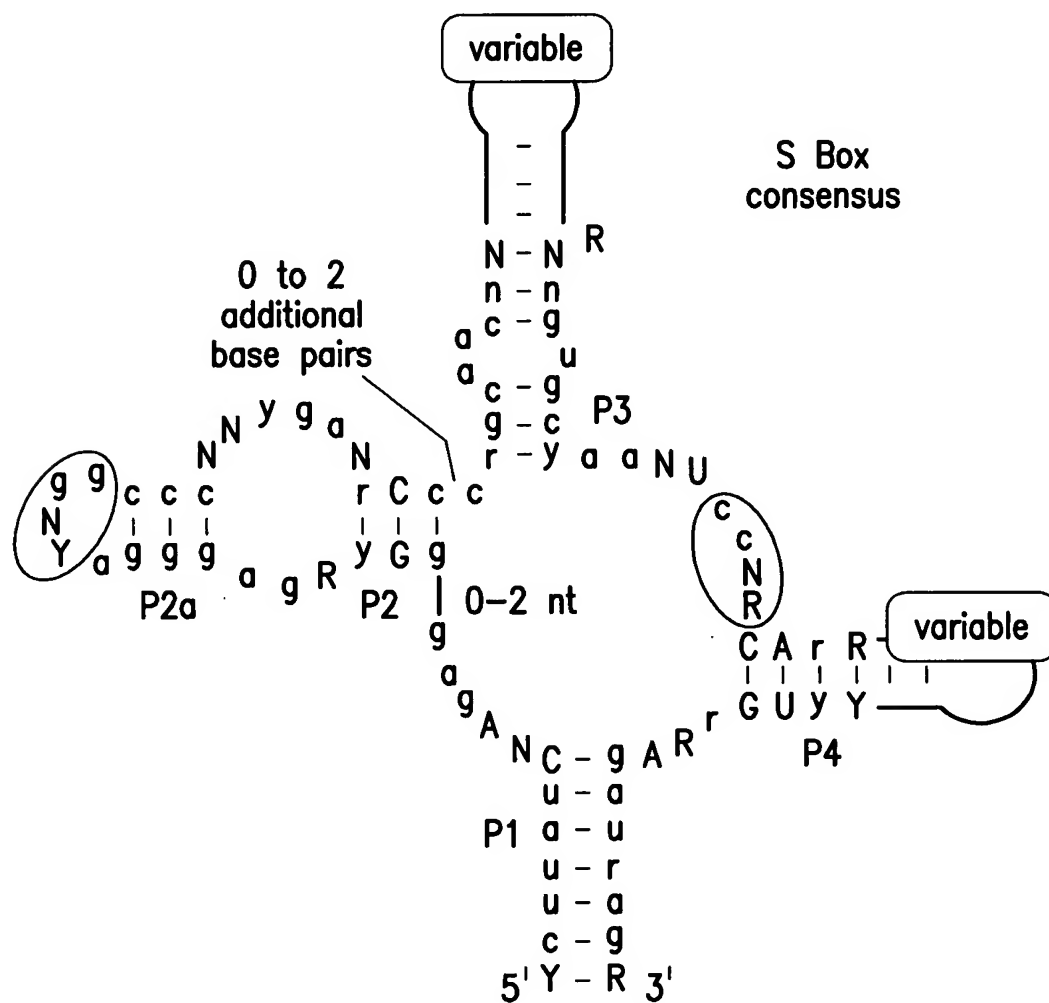


FIG. 30A

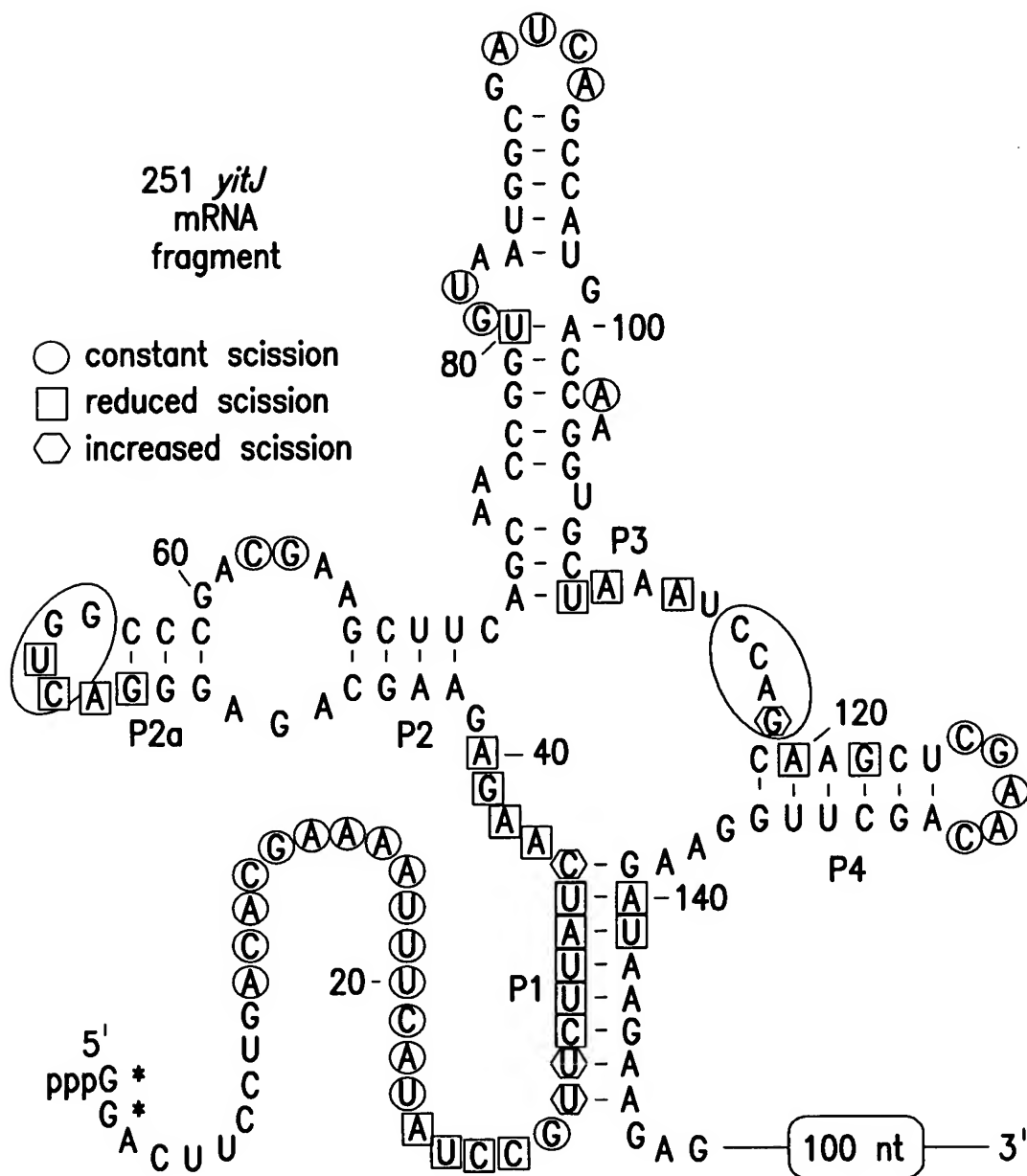


FIG.30B

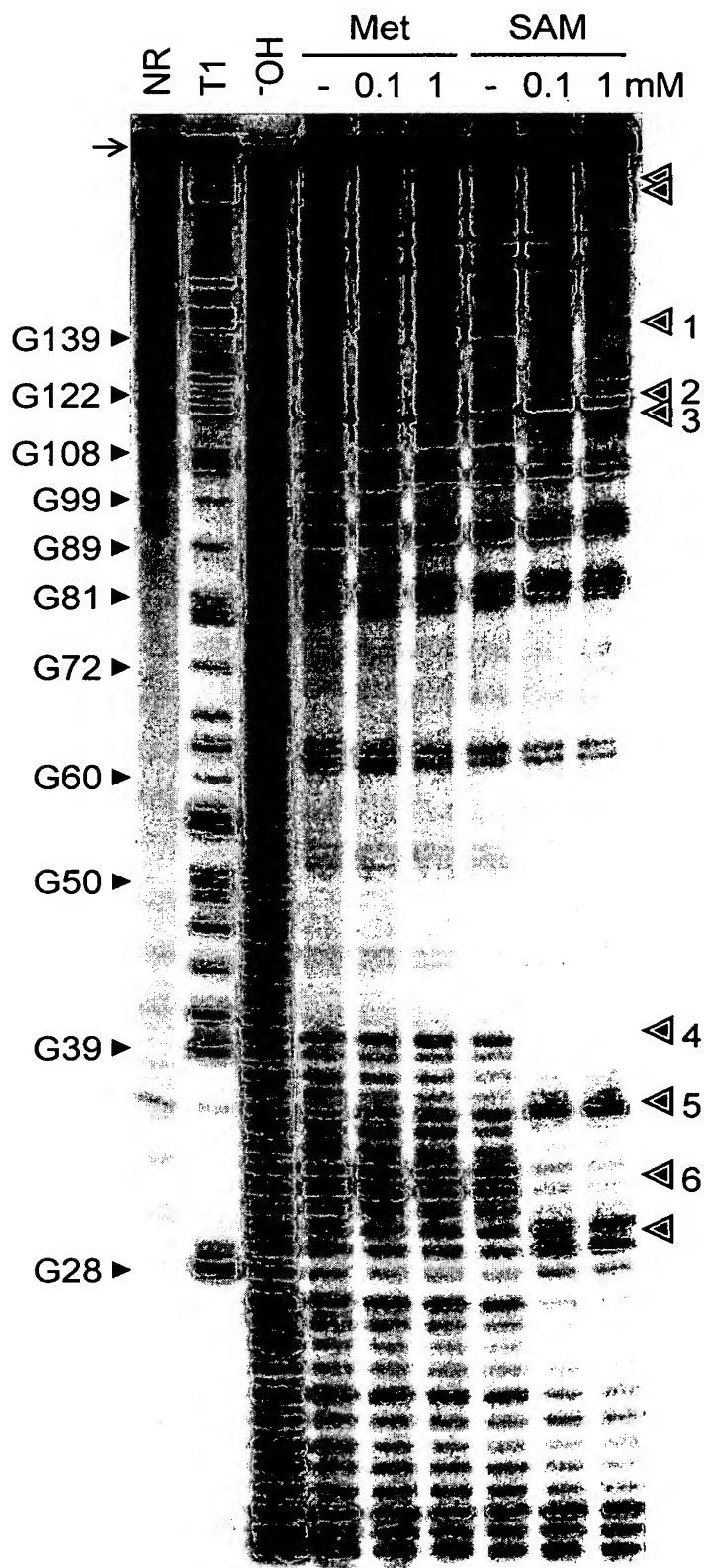


FIG.30C



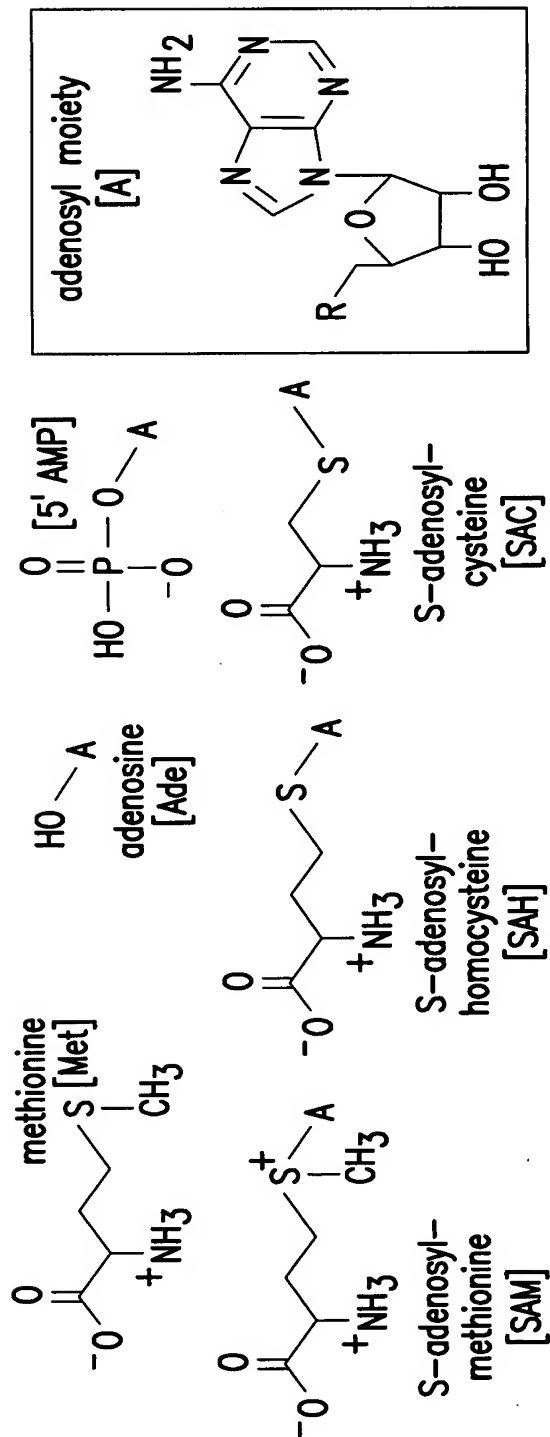


FIG. 31A

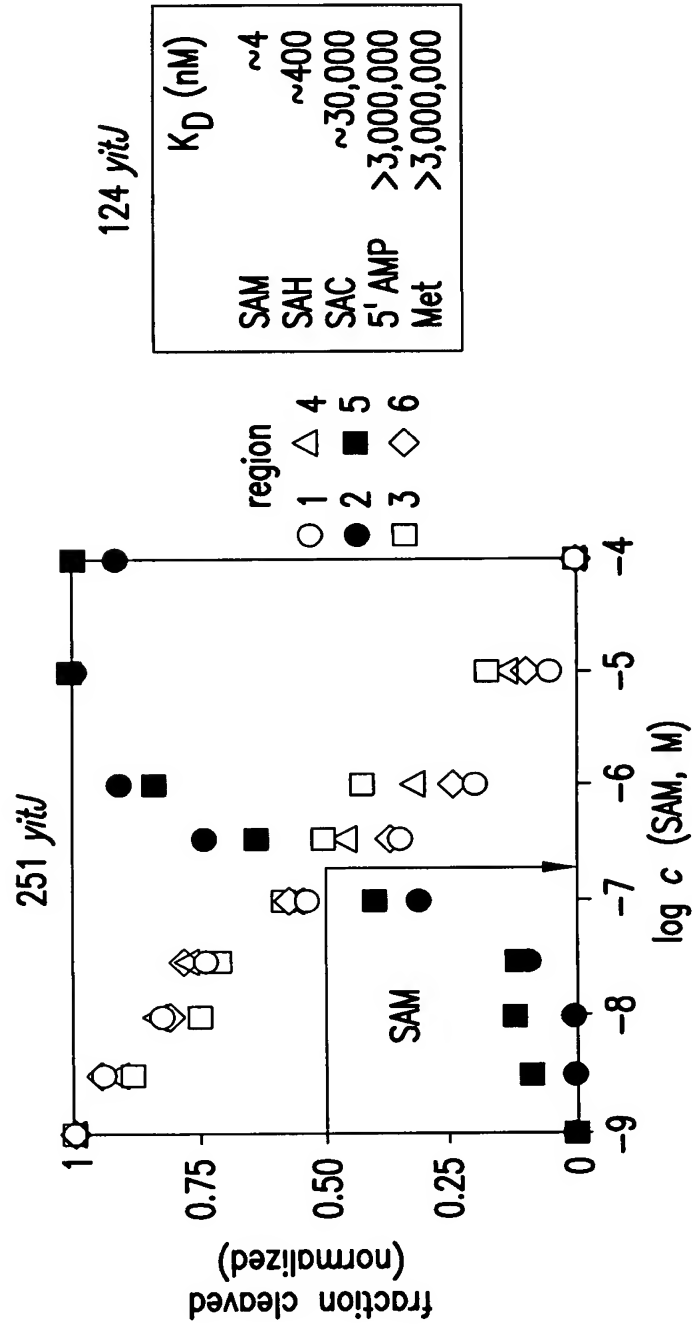


FIG.31B

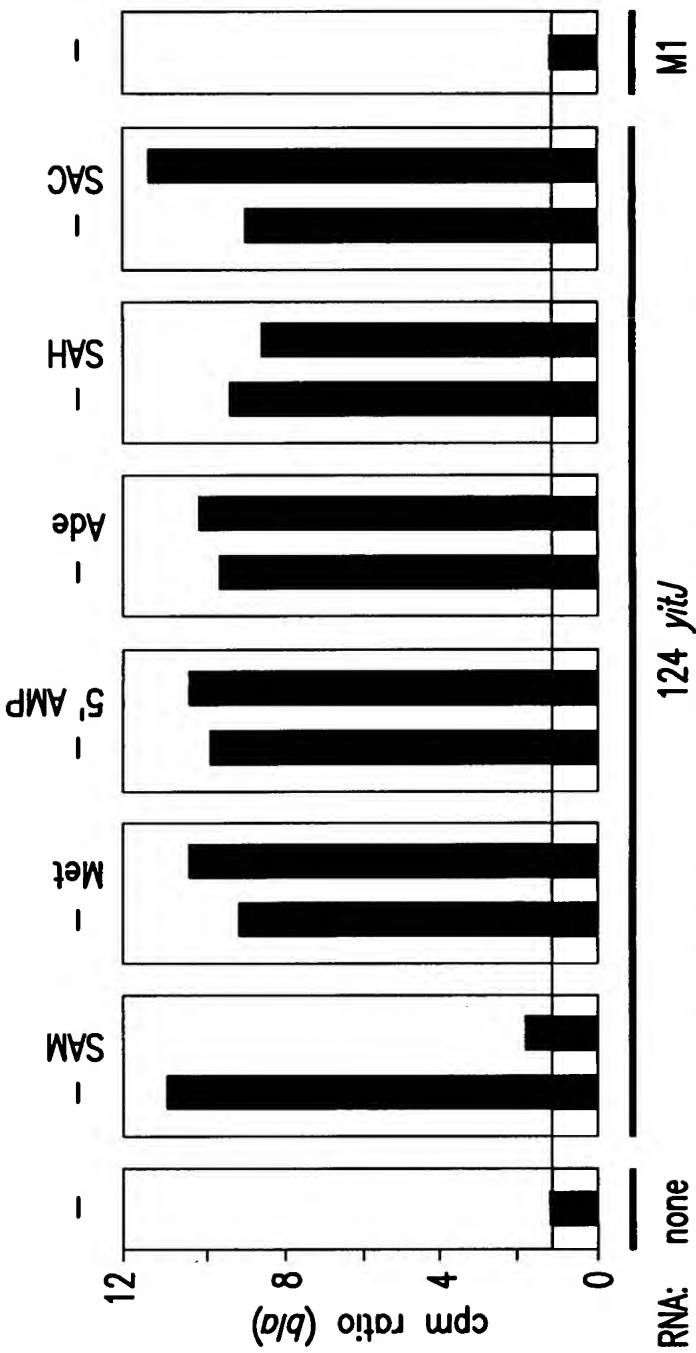


FIG.31C

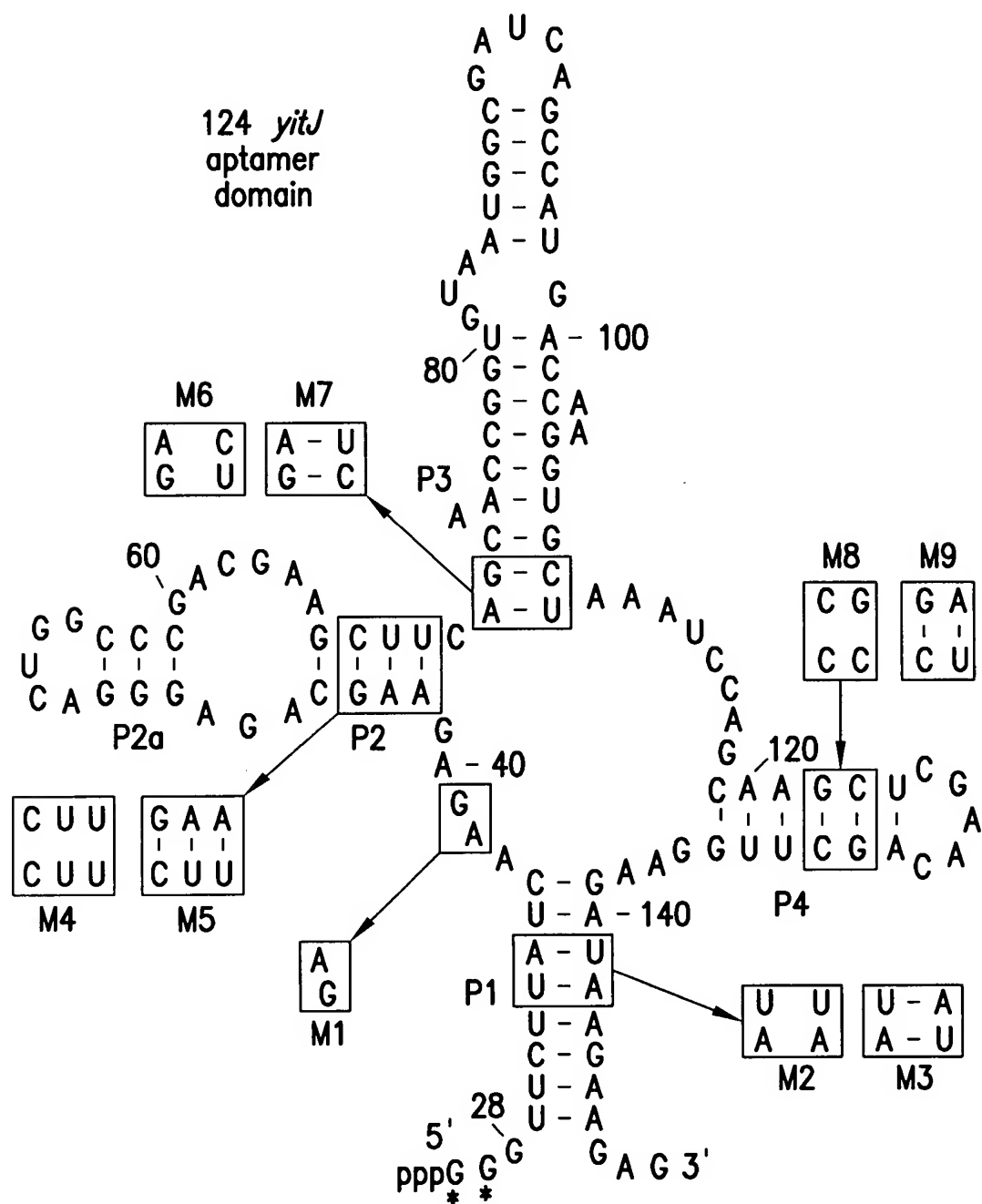


FIG.32A

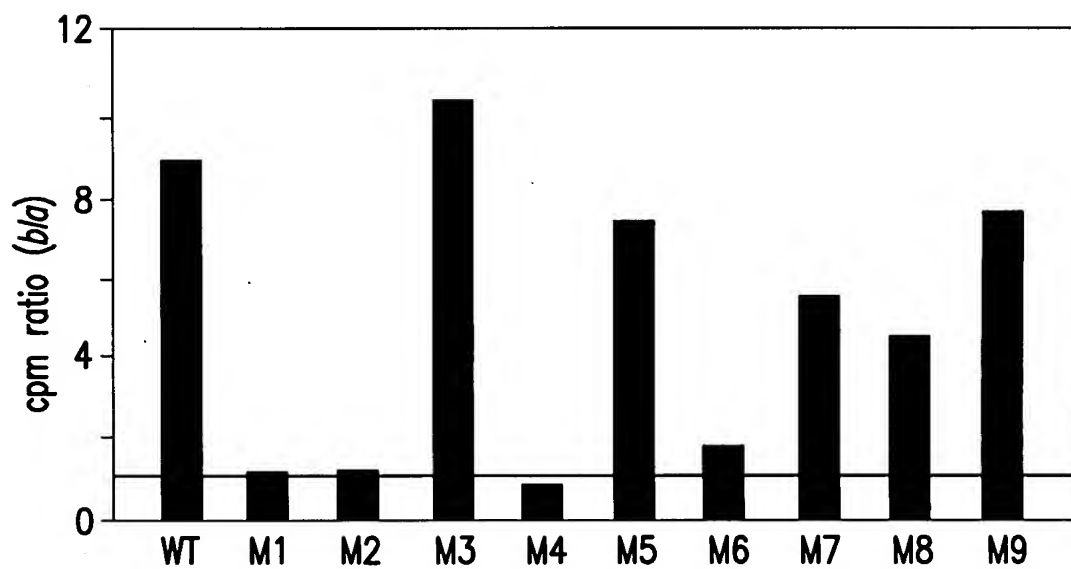


FIG.32B

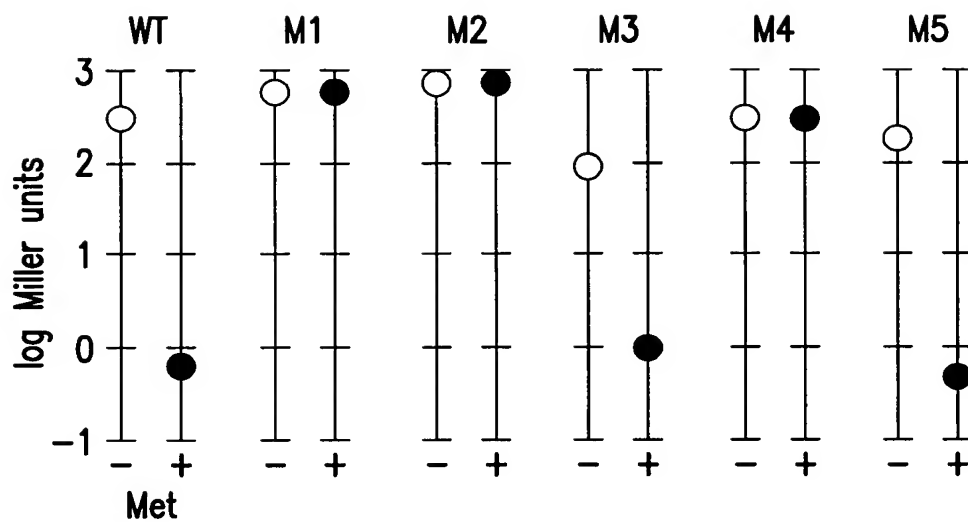


FIG.32C

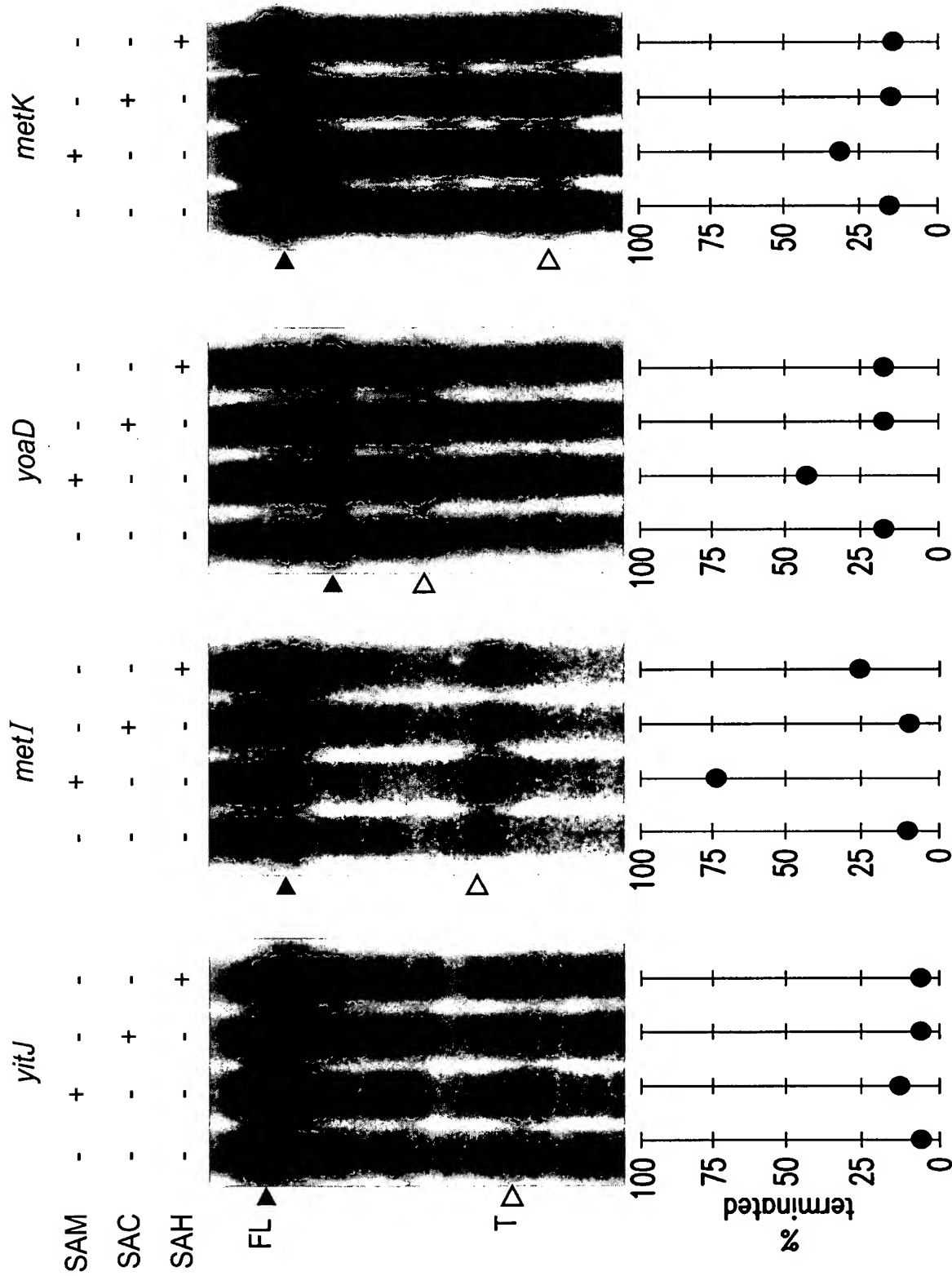


FIG.33A

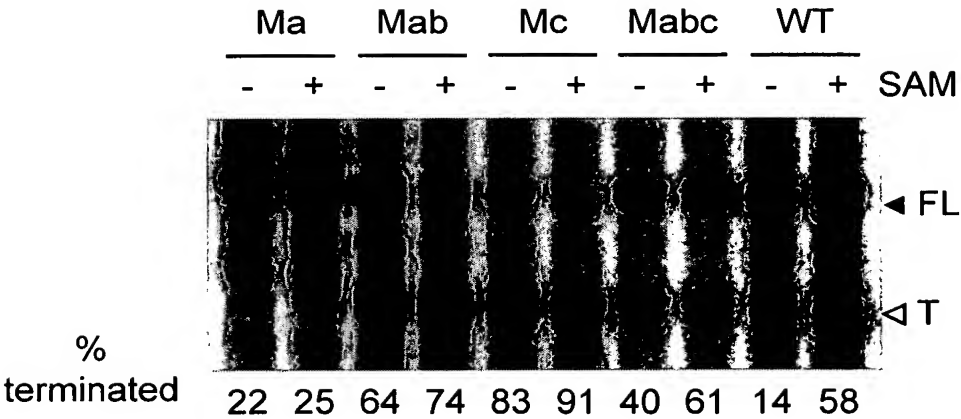


FIG.33B-1





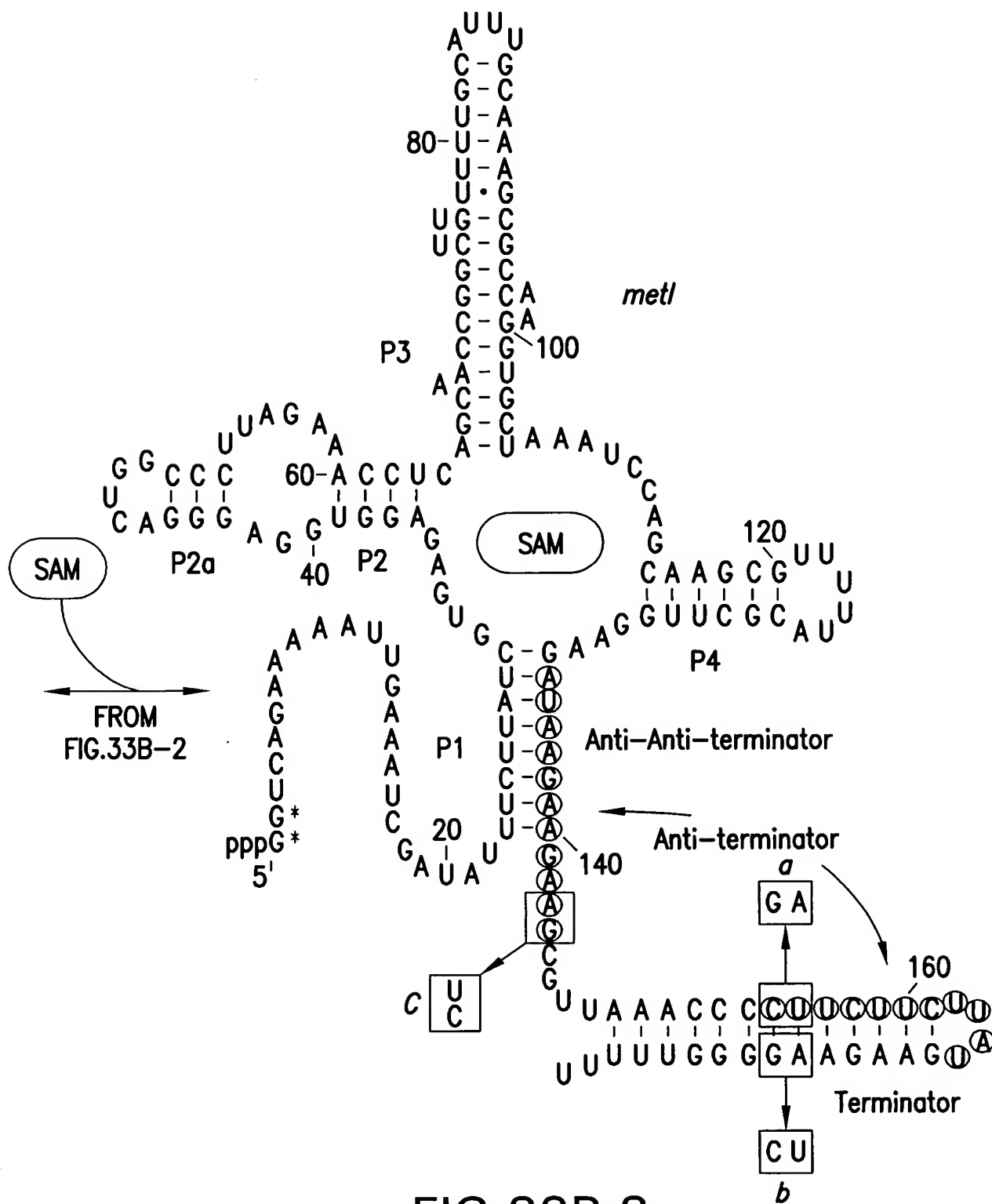
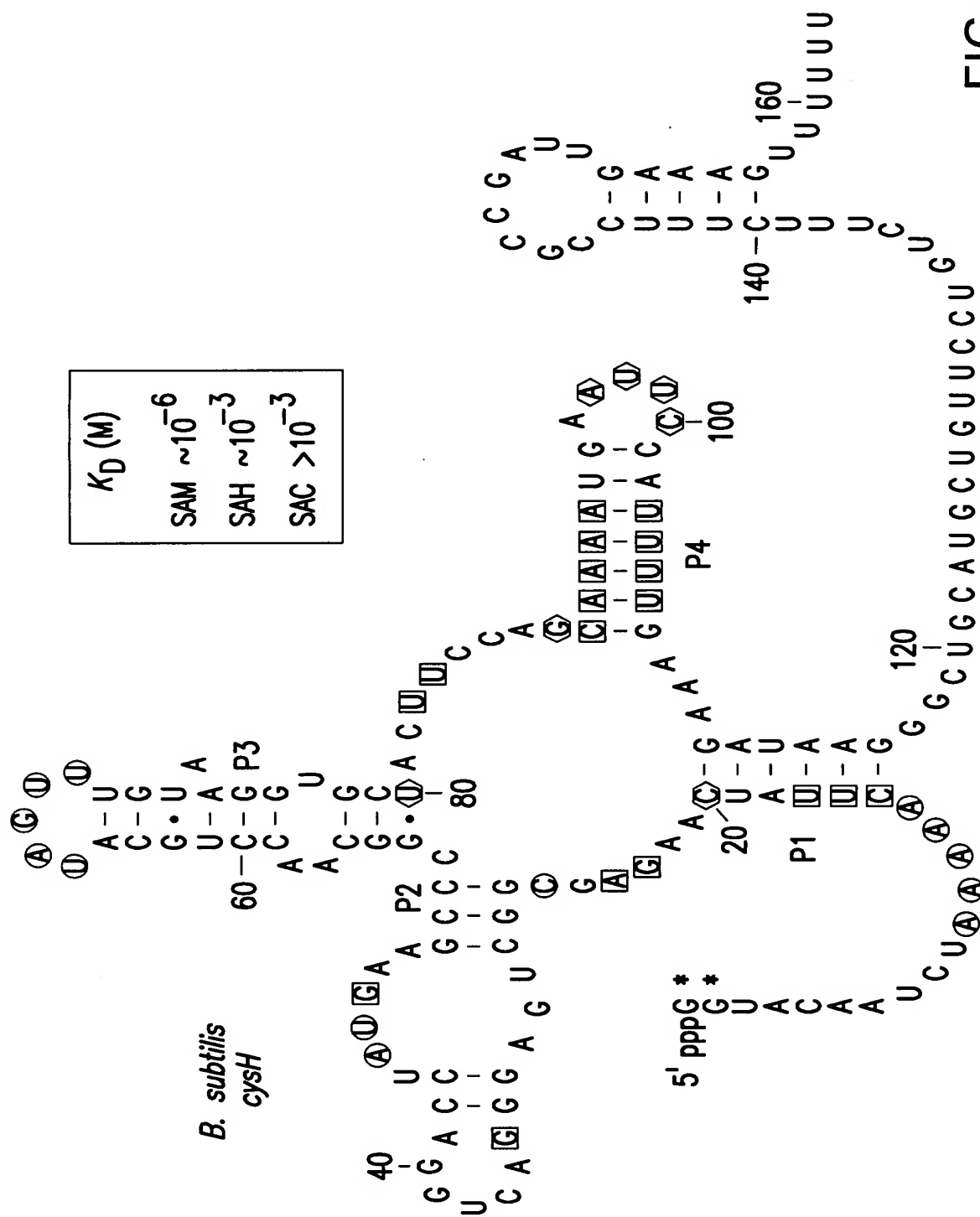


FIG.33B-3



**FIG. 34A**

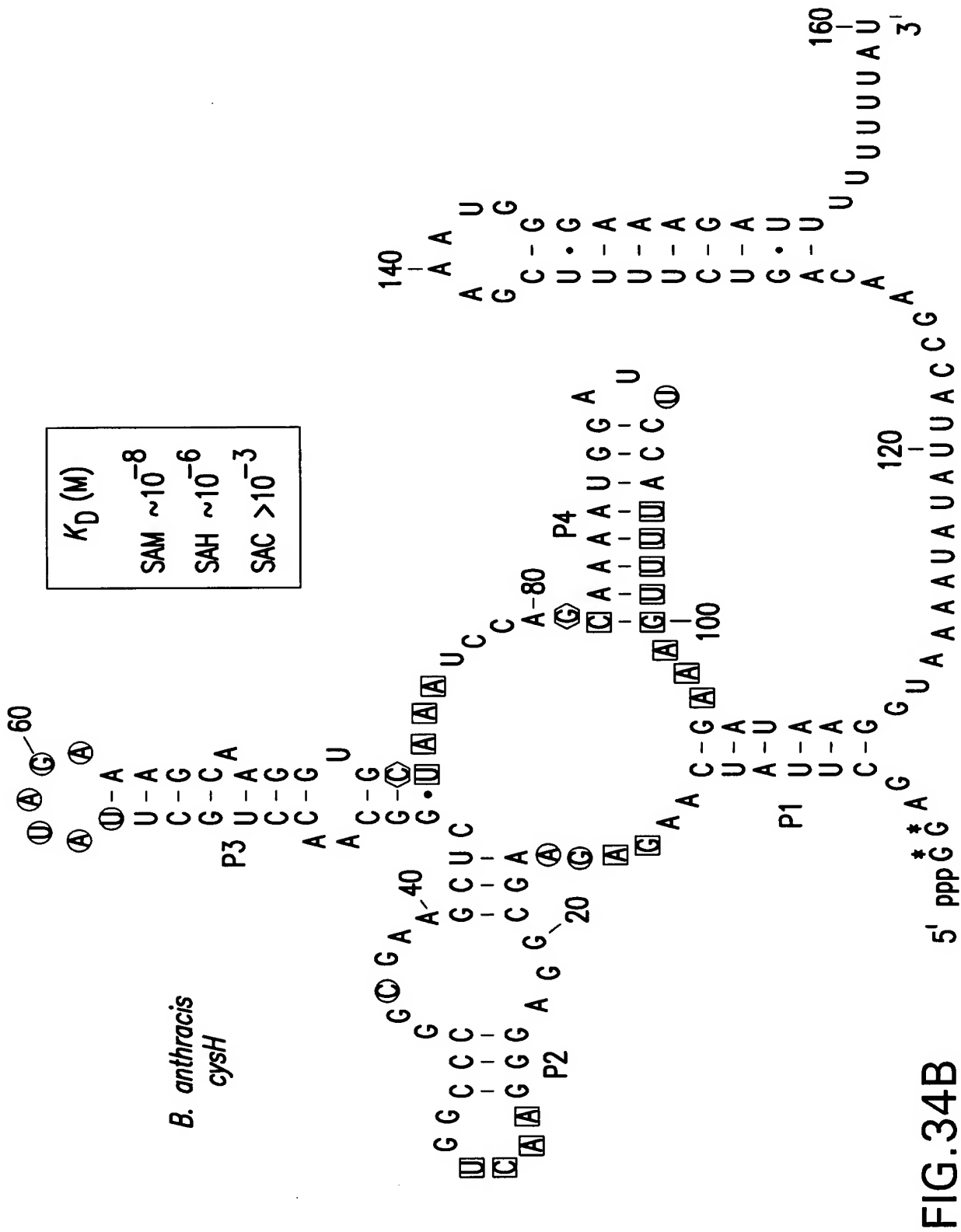


FIG.34B

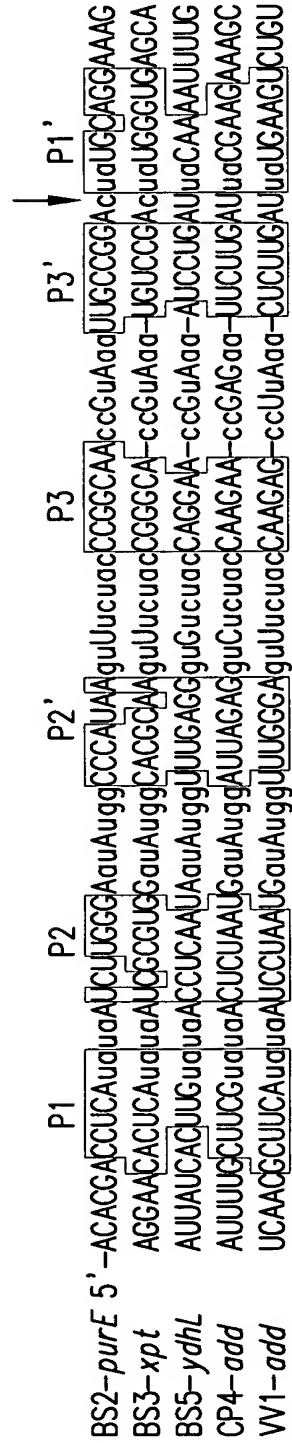


FIG. 35A

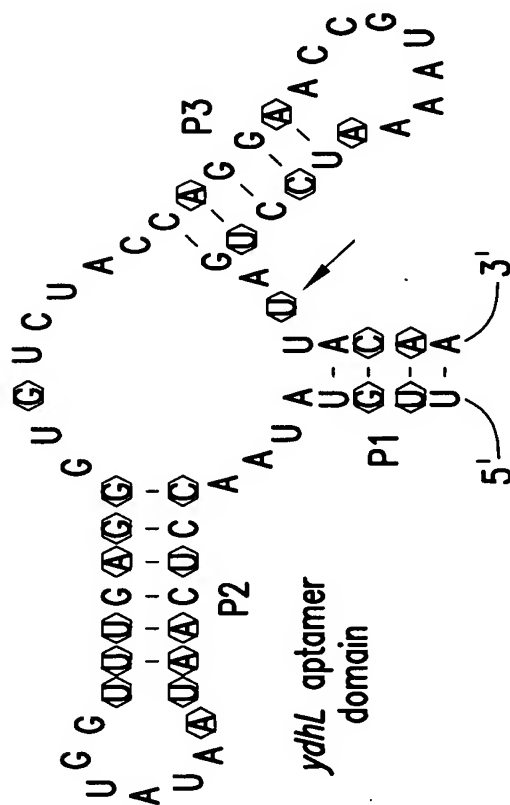


FIG.35C

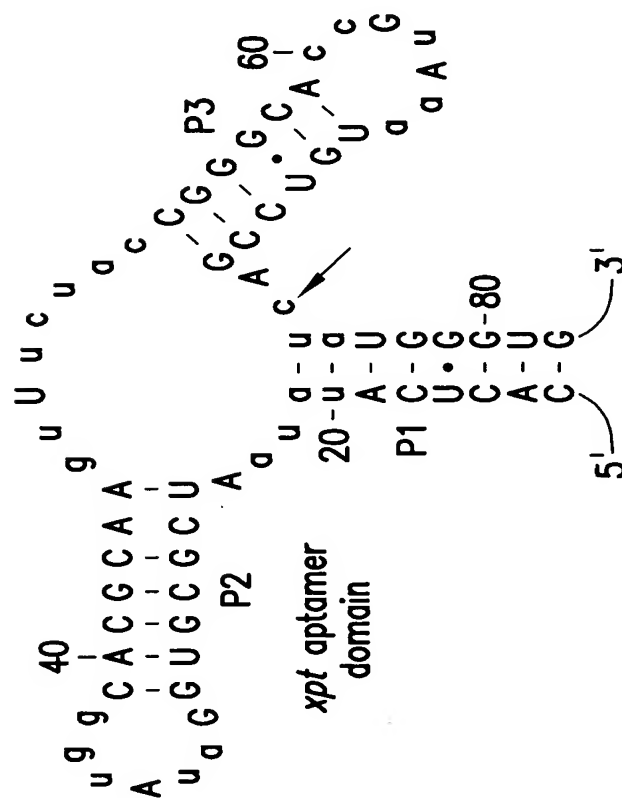


FIG.35B

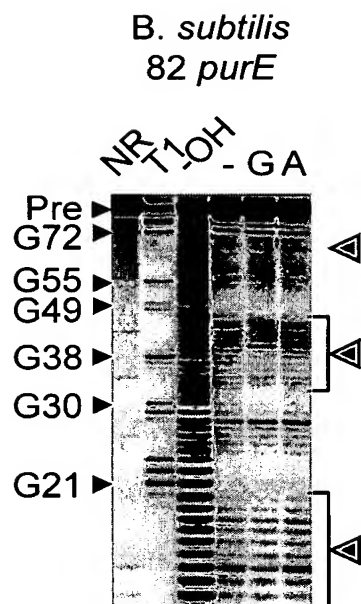


FIG. 36A

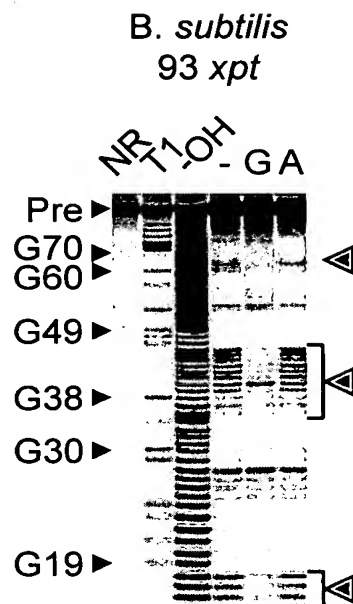


FIG. 36B

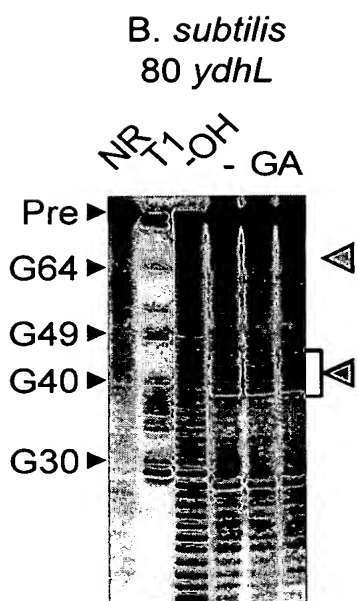


FIG. 36C

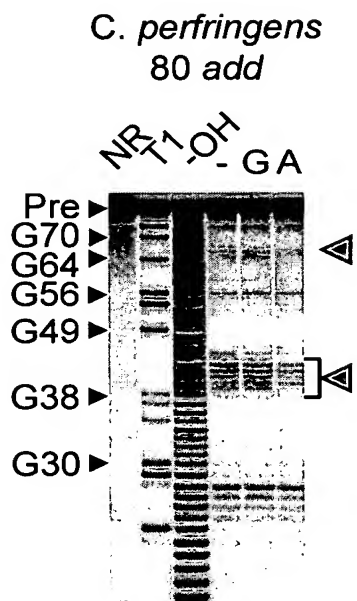


FIG. 36D

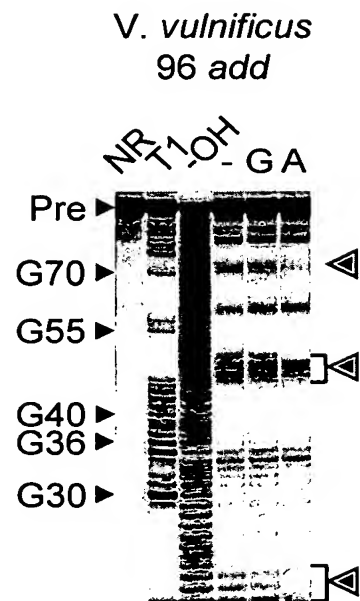


FIG. 36E

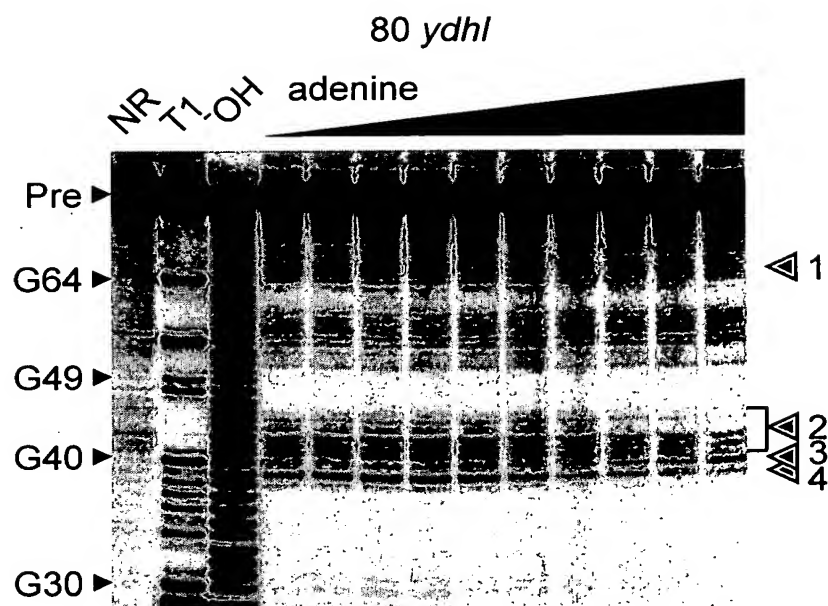


FIG.37A

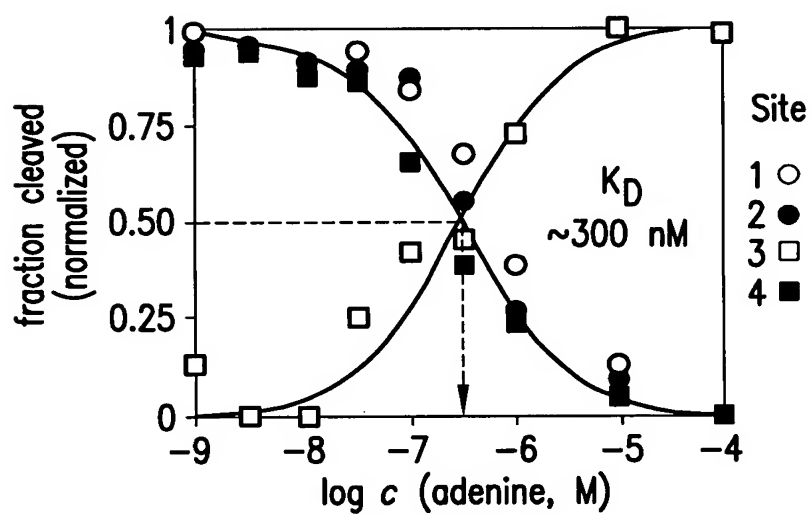


FIG. 37B



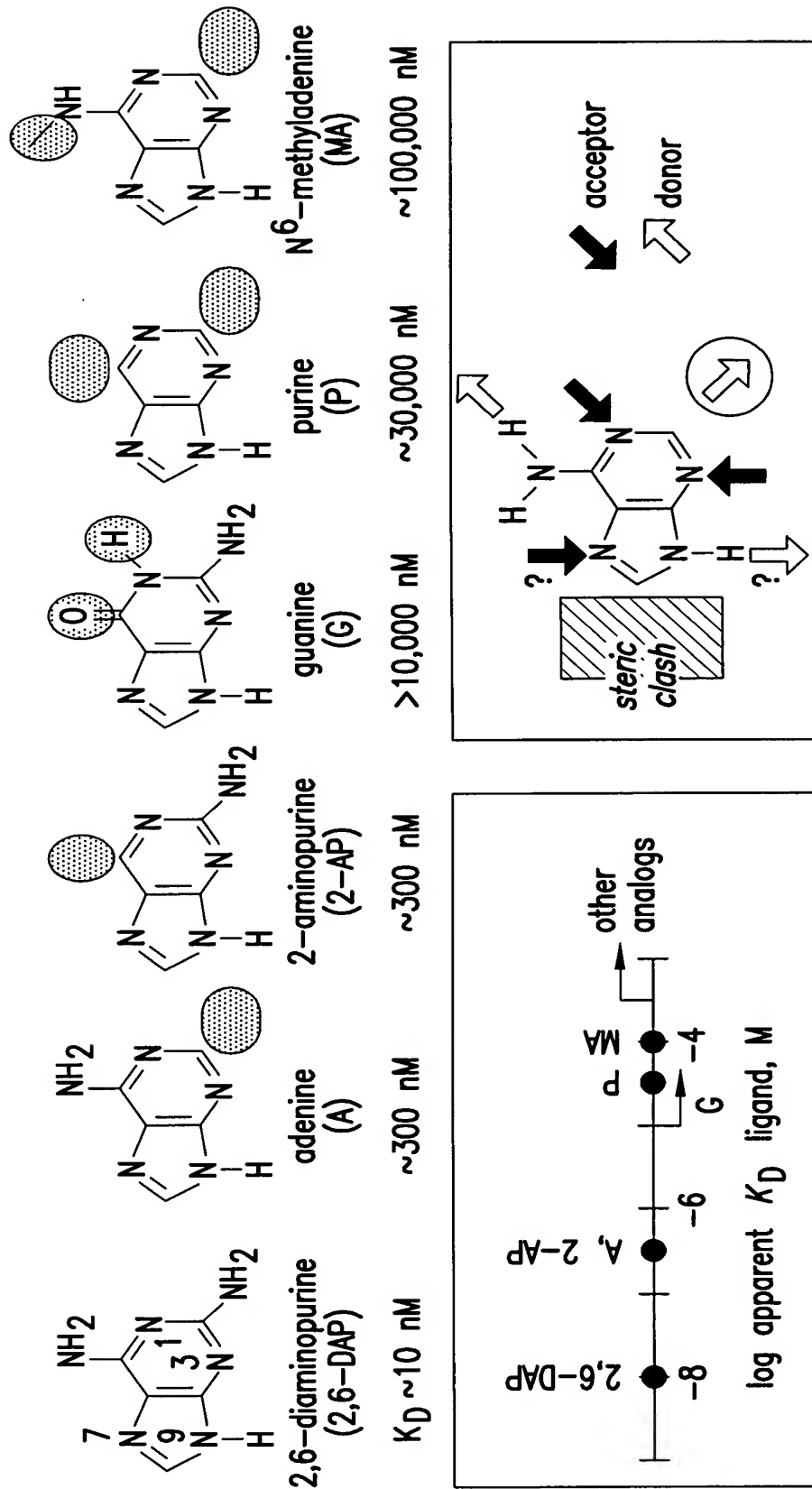


FIG.38A

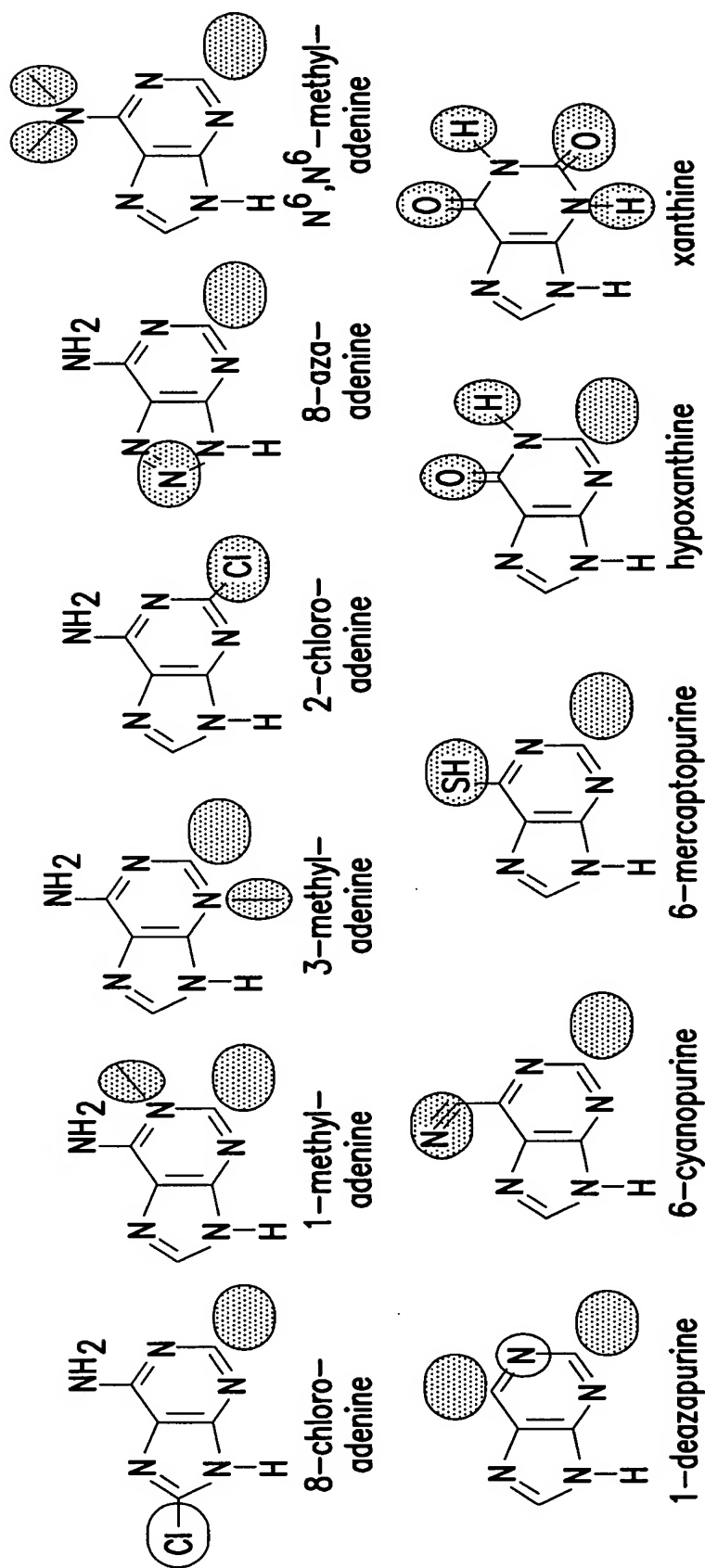


FIG. 38B

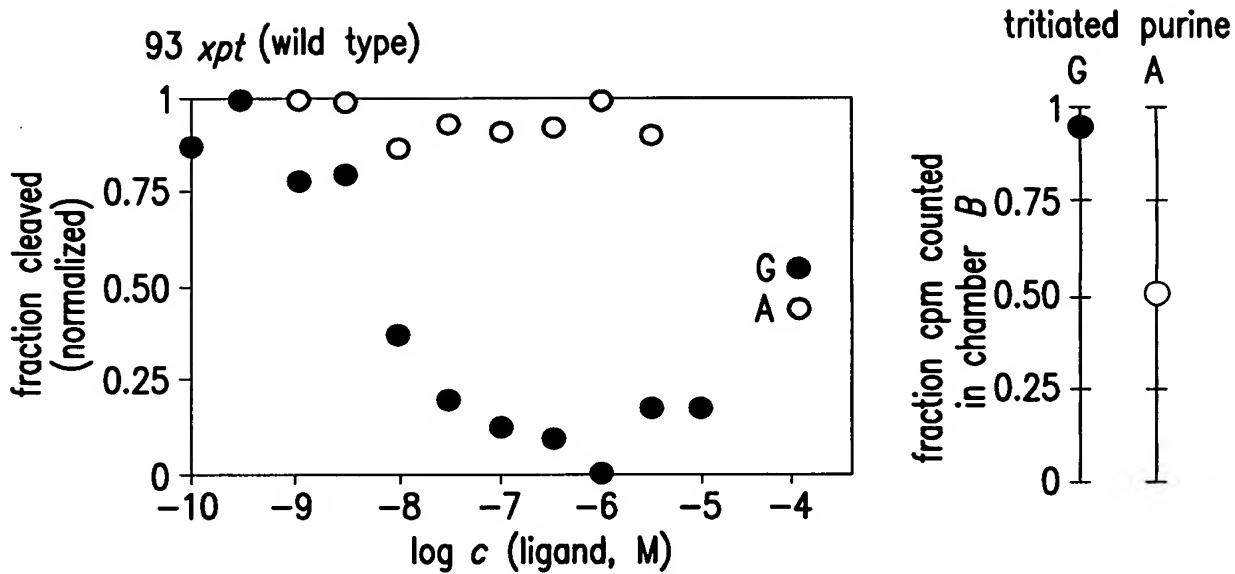


FIG. 39A

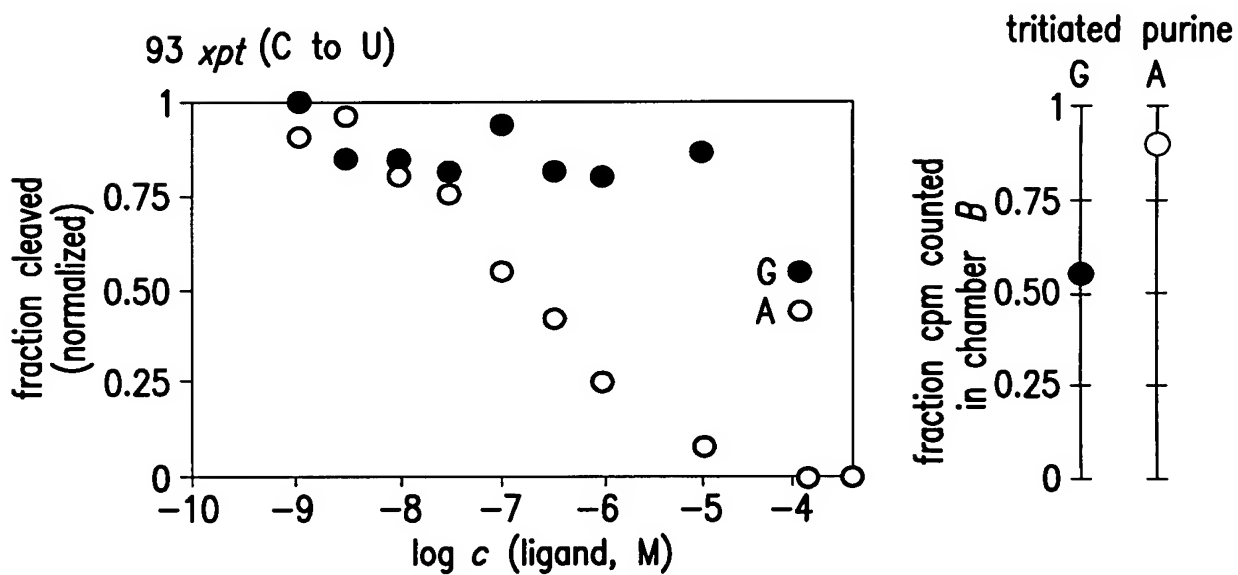


FIG. 39B

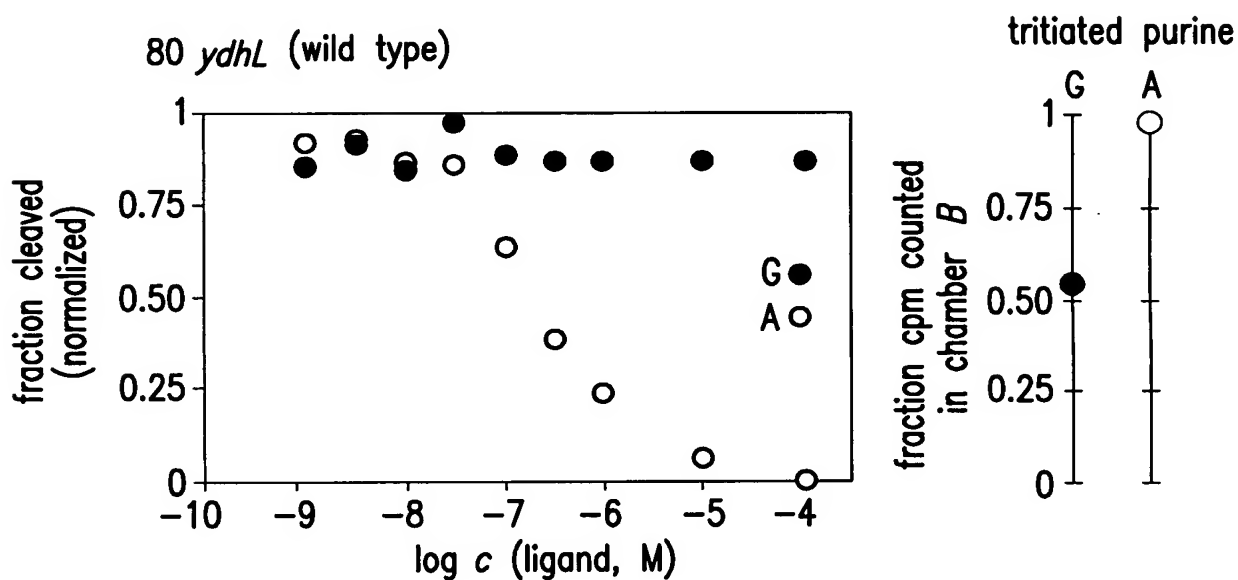


FIG. 39C

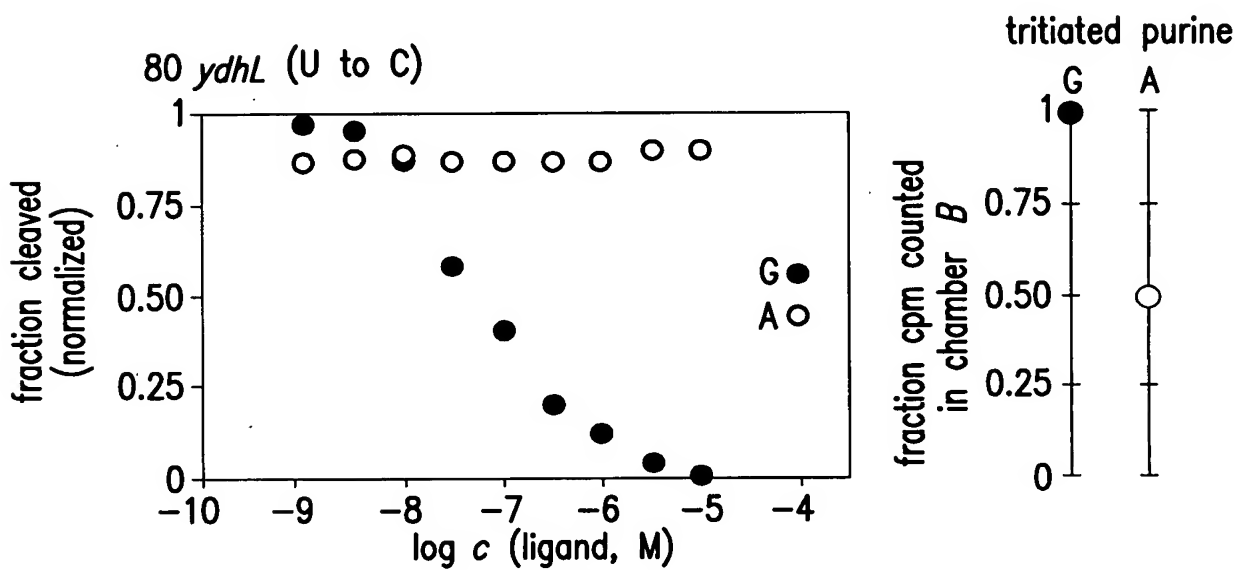


FIG. 39D

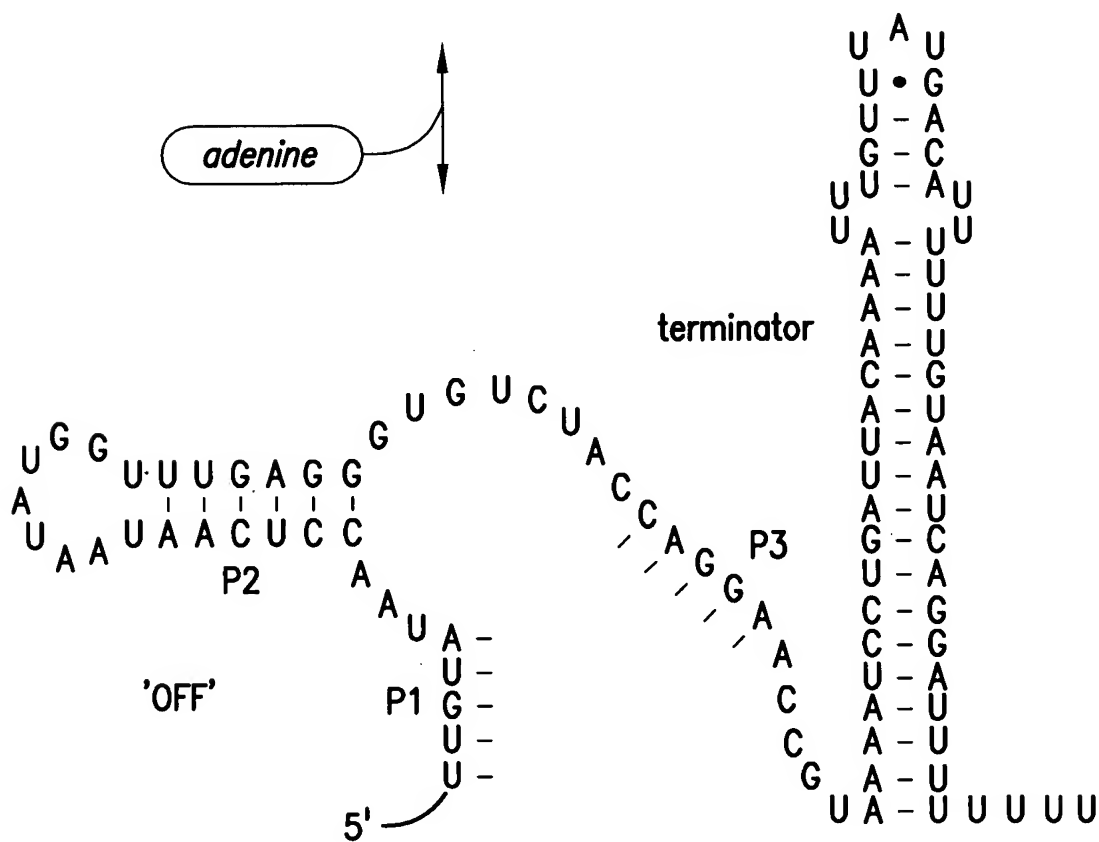
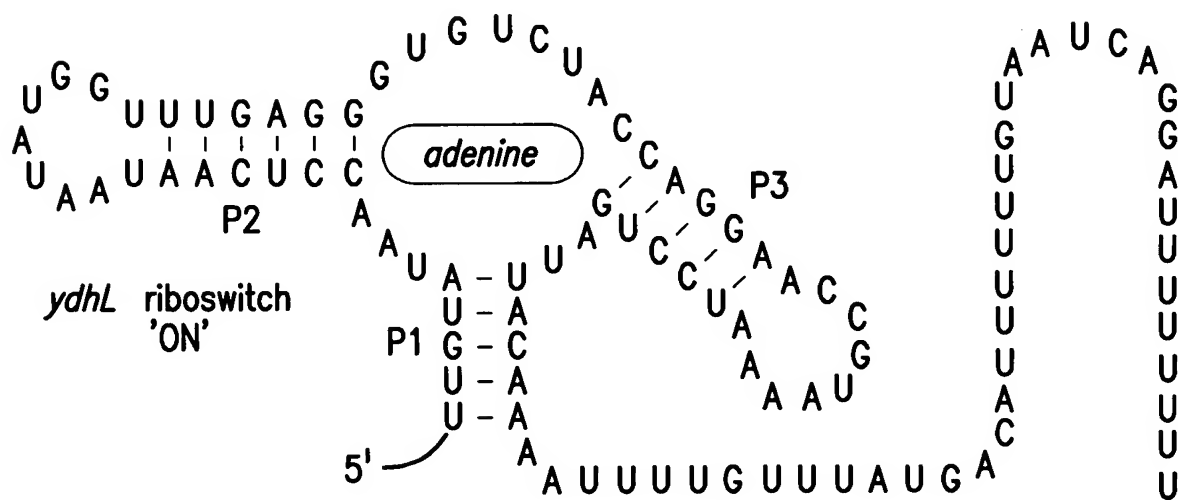


FIG.40A

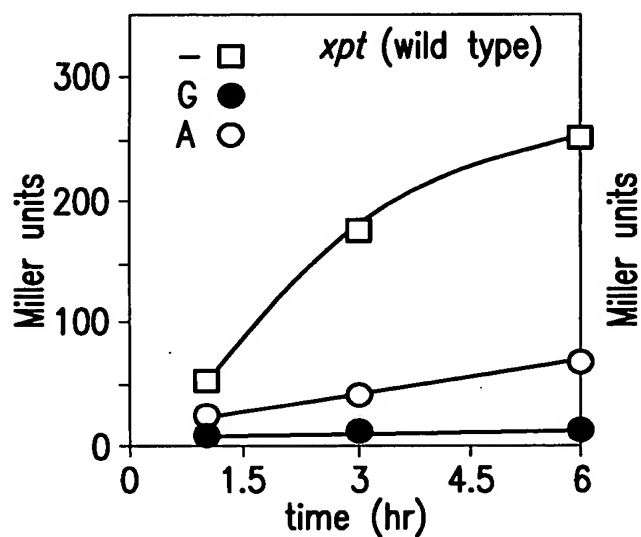


FIG. 40B

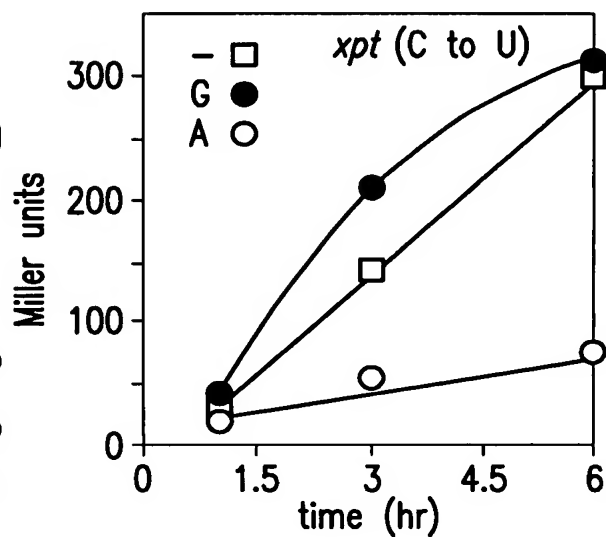


FIG. 40C

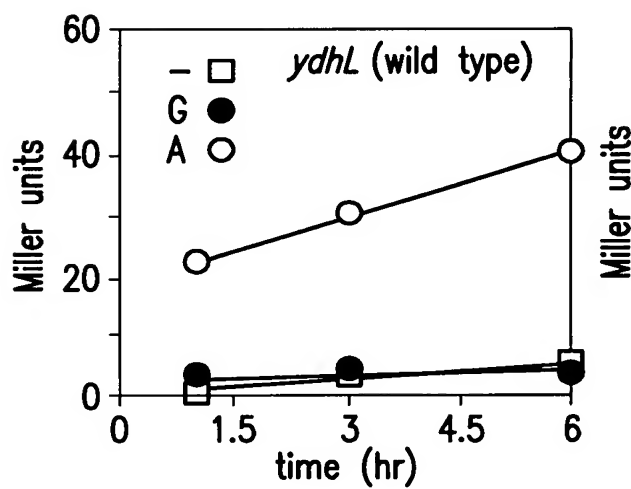


FIG. 40D

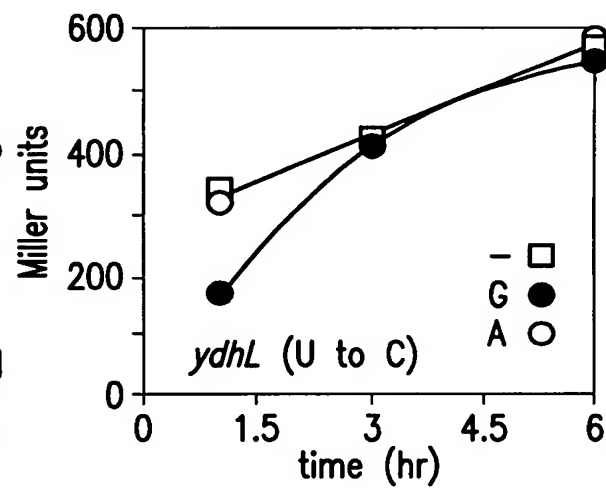


FIG. 40E

A. Alignment of SAM Riboswitches.

Table S1. S Box Sequence Alignment

ID	Position	Genbank Acc.	Organism	Remark	Start	Operon
Bs01	-	1180274	NC_000964.1	Bacillus subtilis	92	metF (yitJ)
Bs02	+	1257777	NC_000964.1	Bacillus subtilis	70	metB-metC (yjcI)
Bs03	-	1385353	NC_000964.1	Bacillus subtilis	130	metE (metC)
Bs04	-	1424147	NC_000964.1	Bacillus subtilis	89	ykrT-GCN3 (ykrT)
Bs05	+	1426344	NC_000964.1	Bacillus subtilis	60	rbcl-ykrX-araD-ykrZ (ykrW)
Bs06	+	1629516	NC_000964.1	Bacillus subtilis	164	cysH-pitA-MET3-cysC (cysH)
Bs07	-	2024504	NC_000964.1	Bacillus subtilis	86	ldhA-xyIB (yodD)
Bs08	-	3128412	NC_000964.1	Bacillus subtilis	170	metK (metE)
Bs09	-	3363560	NC_000964.1	Bacillus subtilis	108	abc -2011-nlpA (yusC)
Bs10	+	3996569	NC_000964.1	Bacillus subtilis	85	metE (yxjH)
Bs11	+	3997959	NC_000964.1	Bacillus subtilis	80	metE (yxjG)
Bh01	-	910190	NC_002570.1	Bacillus halodurans	141	???
Bh02	+	1348818	NC_002570.1	Bacillus halodurans	99	thrA
Bh03	+	1699959	NC_002570.1	Bacillus halodurans	175	metB-metC-metF-methH

FIG.41-1

Bh04	-	3427466	NC_002570.1	Bacillus halodurans	157	metK
Bh05	-	3591166	NC_002570.1	Bacillus halodurans	220	abc -2011-nlpA
Oi01	+	727028	NC_004193.1	Oceanobacillus iheyensis	78	meth
Oi02	-	1098097	NC_004193.1	Oceanobacillus iheyensis	162	metE
Oi03	+	1319043	NC_004193.1	Oceanobacillus iheyensis	76	???
Oi04	-	2134364	NC_004193.1	Oceanobacillus iheyensis	56	abc -???-nlpA
Oi05	-	2365511	NC_004193.1	Oceanobacillus iheyensis	176	metK
Oi06	-	2437305	NC_004193.1	Oceanobacillus iheyensis	129	abc -???-nlpA
Oi07	-	2708643	NC_004193.1	Oceanobacillus iheyensis	177	tran-MET17
Oi10	-	3200636	NC_004193.1	Oceanobacillus iheyensis	81	???-???
Oi08	-	2856863	NC_004193.1	Oceanobacillus iheyensis	201	???-???
Oi09	+	3162075	NC_004193.1	Oceanobacillus iheyensis	105	MET17
Oi10	-	3200636	NC_004193.1	Oceanobacillus iheyensis	81	???-???
Oi11	+	3200766	NC_004193.1	Oceanobacillus iheyensis	94	???
Oi12	+	3294474	NC_004193.1	Oceanobacillus iheyensis	97	abc-2011-nlpA-abgB
Oi13	-	3466518	NC_004193.1	Oceanobacillus iheyensis	112	gldA-nlpA-abc-2011
Ca01	+	453565	NC_003030.1	Clostridium acetobutylicum	78	metB-metC
Ca02	-	671354	NC_003030.1	Clostridium acetobutylicum	77	meth
Ca03	-	1073886	NC_003030.1	Clostridium acetobutylicum		(smtA-metB-cysK)
Ca04	+	1131539	NC_003030.1	Clostridium acetobutylicum	81	abc-2011-nlpA

(1)

(2)

FIG.41-2



Ca05	+	1976373	NC_003030.1	Clostridium acetobutylicum			102	metA
Ca06	-	2914839	NC_003030.1	Clostridium acetobutylicum			117	CAC5
Ca07	-	2991405	NC_003030.1	Clostridium acetobutylicum			70	metK
Cp01	-	2500081	NC_003366.1	Clostridium perfringens			391	metK
Cp02	-	2665229	NC_003366.1	Clostridium perfringens			102	rhaC
Lm01	+	137135	NC_003210.1	Listeria monocytogenes			90	oppA-dppB-dppC
Lm02	-	309383	NC_003210.1	Listeria monocytogenes			113	nlpA-abc-2011
Lm03	-	637924	NC_003210.1	Listeria monocytogenes			111	MET17-MET2
Lm04	+	882772	NC_003210.1	Listeria monocytogenes			97	metE
Lm05	-	1716649	NC_003210.1	Listeria monocytogenes			110	metK
Lm06	-	1739595	NC_003210.1	Listeria monocytogenes			109	metE-metB-metC-metH
Lm07	-	2491174	NC_003210.1	Listeria monocytogenes			93	abc-2011-nlpA
Li01	+	172401	NC_003212.1	Listeria innocua	(*)		88	oppA-dppB-dppC
Li02	-	327333	NC_003212.1	Listeria innocua	(*)		113	nlpA-abc-2011
Li03	-	636911	NC_003212.1	Listeria innocua	(*)		111	met17-met2
Li04	+	871751	NC_003212.1	Listeria innocua	(*)		97	metE
Li05	-	1772459	NC_003212.1	Listeria innocua	(*)		110	metK
Li06	-	1790189	NC_003212.1	Listeria innocua	(*)		109	metE-metB-metC-metH
Li07	-	2538251	NC_003212.1	Listeria innocua	(*)		92	abc-2011-nlpA
Sa01	+	15958	NC_002745.1	Staphylococcus aureus			41	met2

FIG.41-3

Sa02	+	875385	NC_002745.1	Staphylococcus aureus	91	abc-2011-nlpA
Sa03	-	1844603	NC_002745.1	Staphylococcus aureus	108	metK
Sa04	-	2381620	NC_002745.1	Staphylococcus aureus	13	rhaC
Sc01	+	4708438	NC_003888.1	Streptomyces coelicolor	26	thrC-moaD

FIG.41-4

ID	Position	Genbank Acc.	Organism	Remark	Start	Operon
Ct01	+	606192	AE_006470	Chlorobium tepidum	107	CAC5-MET2
Tt01	+	500245	NC_003869.1	Thermoanaerobacter tengcongensis	55	metK
Tt02	-	1750367	NC_003869.1	Thermoanaerobacter tengcongensis	66	metF-methH-ebsC
Tt03	-	2076680	NC_003869.1	Thermoanaerobacter tengcongensis	78	thrA-CAC5
Fn01	-	987483	NC_003454.1	Fusobacterium nucleatum	84	metK
Fn02	-	1317650	NC_003454.1	Fusobacterium nucleatum	91	abc-2011-nlpA
Dr01	+	1363063	NC_001263.1	Deinococcus radiodurans, chr 1	156	abc-2011-nlpA-nlpA
Dr02	+	980704	NC_001263.1	Deinococcus radiodurans, chr 1	41	meth-???-metF
Xa01	-	3558018	NC_003919.1	Xanthomonas axonopodis	74	MET2-metC-thrA
Xc01	-	3379769	NC_003902.1	Xanthomonas campestris	73	MET2-metC-thrA
Se01	+	574	AF_269983.1	Staphylococcus epidermidis genomic clone		
Se02	-	142	AF_270301.1	Staphylococcus epidermidis genomic clone		
Gs01	+	342843	contig:2947	Geobacter sulferreducens		
Gs02	+	2470946	contig:2947	Geobacter sulferreducens		
Ba01	-	177272	contig:6615	Bacillus anthracis		
Ba02	+	185586	contig:6615	Bacillus anthracis		
Ba03	-	197185	contig:6615	Bacillus anthracis		
Ba04	+	320607	contig:6615	Bacillus anthracis		

FIG.41-5

Ba05	-	371127	contig:6615	Bacillus anthracis	(*)
Ba06	+	1362659	contig:6615	Bacillus anthracis	
Ba07	+	1375353	contig:6615	Bacillus anthracis	
Ba08	+	2459362	contig:6615	Bacillus anthracis	
Ba09	-	2953226	contig:6615	Bacillus anthracis	
Ba10	-	3091676	contig:6615	Bacillus anthracis	
Ba11	-	3890736	contig:6615	Bacillus anthracis	
Ba12	+	3892933	contig:6615	Bacillus anthracis	
Ba13	+	4074285	contig:6615	Bacillus anthracis	
Ba14	-	4074078	contig:6615	Bacillus anthracis	
Ba15	-	4553682	contig:6615	Bacillus anthracis	
Ba16	-	4739975	contig:6615	Bacillus anthracis	
Ba17	-	5140322	contig:6615	Bacillus anthracis	
Bc01	+	26115	contig:1617	Bacillus anthracis	(*)
Bc02	+	748841	contig:1617	Bacillus cereus	
Bc03	+	1183078	contig:1617	Bacillus cereus	(*)
Bc04	+	1195849	contig:1617	Bacillus cereus	(*)
Bc05	+	2200884	contig:1617	Bacillus cereus	(*)
Bc06	-	2684484	contig:1617	Bacillus cereus	(*)
Bc07	-	2963724	contig:1617	Bacillus cereus	(*)

FIG.41-6

Bc08	-	2773209	contig:1617	Bacillus cereus	(*)
Bc09	+	3500608	contig:1617	Bacillus cereus	(*)
Bc10	-	3687209	contig:1617	Bacillus cereus	(*)
Bc11	+	3687417	contig:1617	Bacillus cereus	(*)
Bc12	-	3498410	contig:1617	Bacillus cereus	(*)
Bc13	-	4205859	contig:1617	Bacillus cereus	(*)
Bc14	-	4397125	contig:1617	Bacillus cereus	(*)
Bc15	-	4784934	contig:1617	Bacillus cereus	(*)
Bc16	-	5114094	contig:1617	Bacillus cereus	(*)
Bc17	-	5094322	contig:1617	Bacillus cereus	(*)
Bc18	+	5101784	contig:1617	Bacillus cereus	(*)

FIG.41-7

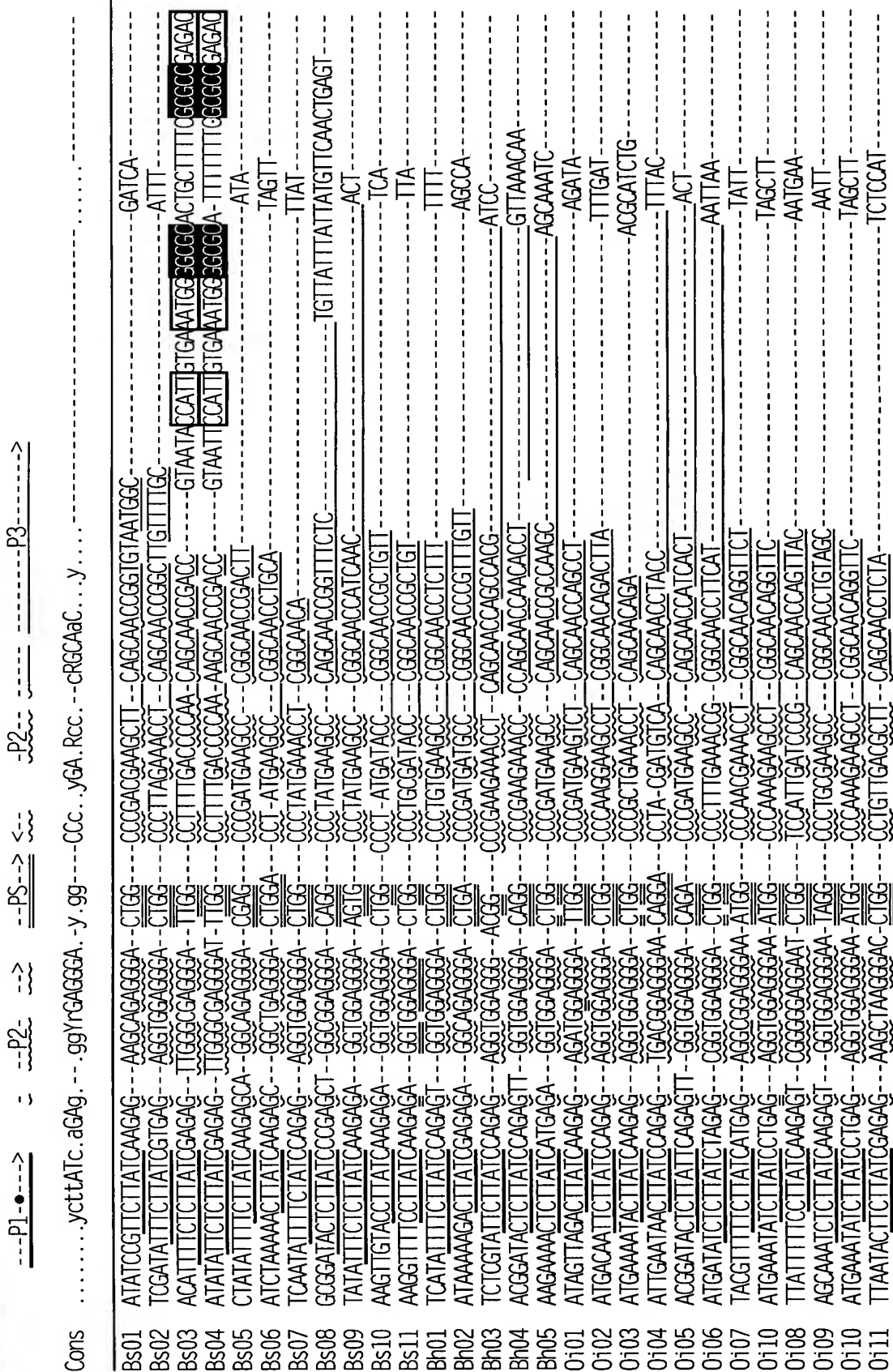


FIG.41-8

Oi12 ACCTTTTCTTCTATGAG--AGATTGAGGGAT--CAGG--CCCTATGACAICI--CGGCAGCGGATICTTTA--TAT-----TAT  
 Oi13 CTAATATCTCTATTGAGAGT--GGCTGAGGGA--CTGG--CCCTGTGAGCC--CGGCAACCGTTTCATCGT--AATCCCA-----  
 Ca01 TAAATTGTTCTTATCAAGAGT--GACGGAGGGA--TAGG--CCCTATGAGTC--CGGCAACATCCAA--TTATT-----  
 Ca02 TGTAAAACTCTATCAAGAGT--GGTGGAGGGA--CTGG--CCCTTTGAACC--CGGCAACCGATATATT--TTT-----  
 Ca03 TAATATTCTCTATCAAGAG--AAACGGAGGGA--CTGG--CCCAATGATGTTI--CAGCAACCAAGGT--TTTAT-----  
 Ca04 ATTAGTGCACCTTATCAAGAGA--GGTGGAGGGA--CCGG--CCCTGTGAAGCC--CAGCAACCTGTATA--TGTTAAT-----  
 Ca05 ATATTATTCTTATCAAGAA--GGTGGAGGGA--CTGG--CCCTATGAAGCC--TGACAAACCGGC--AAAT-----  
 Ca06 TGATAAGGCTCTATCAAGAGA--GGTGGAGGGA--CTGG--CCCTATGAACC--CAACAACCGCATTTI--TTTAATT-----  
 Ca07 ATGGAACCTCTATCAAGAGA--GGTGGAGGGA--AGGG--CCGTTGAAGCC--CGGCAACCGATGTTAT--AATTTA-----  
 Cp01 TTATATACCTCTATCAAGAGA--GGTGGAGGGA--AAGG--CCCTATGAACC--CGGCAACCGATGA--GAAA-----  
 Cp02 TTAATAAATCTTATCAAGAGA--GGTGGAGGGA--CTGG--CCCTGTGAACC--CAGCAACCGGTAAITCTTTGGCGTTAAAAACAATGCTGATTTTAAATAAATAAAAAATCAGT/AGTA  
 Lm01 TTACGTTTCTTATCAAGAGT--GGTGGAGGGA--ATCGG--CCCAGTGAACC--CAGCAGCGGAGC--GCAA-----  
 Lm02 ATATTTCTCTTATCAAGAGC--GGCAGAGGGA--CTGG--CCGATGAAGCC--CGGCAACCTAGCTTTAT--TTAAGC-----  
 Lm03 TAGTATTTCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCTTTGAAGCC--TAGCAACCGGAA--TTTAT-----  
 Lm04 ACATAGTAACCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCGTGAAGCC--TGGCAACCGGA--TTT-----  
 Lm05 AATTATCTCTTATCAAGAGC--GGTAGAGGGA--CTGA--CCCTTTGAAGCC--CAGCAACCTACAC--ATATAA-----  
 Lm06 TAAATTGCTCTTATCAAGT--GGTAGAGGGA--CTGG--CCGTTGAAGCC--CGGCAACCTTTCAA--TACG-----  
 Lm07 TGTAAGAACTCTTATCAAGT--GGTGGAGGGA--AATG--CCCTATGAAGCC--CAGCAACCTAAACAATAA--TTCA-----  
 Li01 TTACAAATTTCTTATCAAGT--GGTGGAGGGA--TCGG--CCCAGTGAACC--CGGCAACCGGAGC--GCAA-----  
 Li02 ATATTTCTCTTATCAAGAGC--GGCAGAGGGA--CTGG--CCGATGAAGCC--CGGCAACCTAGCTTTAT--TTAAGC-----  
 Li03 TAGTATTTCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCTTTGAAGCC--TAGCAACCGGAA--TTTAT-----  
 Li04 ACATAGTAACCTTATCAAGAA--AGGTGGAGGGA--CTGG--CCCAGTGAAGCC--TGGCAACCGGA--CTTT-----  
 Li05 AATTATCTCTTATCAAGAGC--GGTAGAGGGA--CTGA--CCCTTTGAAGCC--CAGCAACCTACAC--ATATAA-----  
 Li06 TAAATTACTCTTATCAAGT--GGTAGAGGGA--CTGG--CCGTTGAAGCC--CAGCAACCTTTCAA--TTCG-----  
 Li07 TGTAAGAACTCTTATCAAGT--GGTGGAGGGA--AATG--CCCTGTGAAGCC--CAGCAACCTAAACAATAA--TTCA-----  
 Sa01 TTCATATTCTTATGAG--AAGTTGAGGGA--TTGG--CCCTGTGATCTI--CAGCAACCGACT--TTAT-----  
 Sa02 CGGTAACCTCTTATCAAGT--GGTGGAGGGA--TTGG--CCCTACGAGCC--CGGCAACCGCTI--ATATA-----  
 Sa03 ACGGATCTCTTATCAAGT--GGTGGAGGGA--ATGG--ACCAATGAAGCC--CAGCAACCTCTTTI--TTTAT-----  
 Sa04 TAAGCATCACTTATCAAG--AGGTGGAGGGA--CTGG--CCCTATGAAGCC--CGGCAACAT--CTOGA-----  
 Sc01 TTCATACCGCTCTATCAAG--GGCAGAGGGA--ACGG--CCCGATGAAGCC--CGGCAACCTCCAGTCGG--TCTTCTGTCACACGGGACGTGGCGGAGCTC--

FIG. 41-9

Cons	.....ycttATc.aGAg.---	ggYrGAGGGA.-y.gg	Ccc..yGA.Rcc.---	cRGCAc...y.....
Ct01	TTTCGAGCTATCATCCAGAA	AGGCGGAGGGA-CTGG	CCCTGGGAAGCCT	TGGCAACCTTCAT
Tt01	TAAACGGCTCTATCAAGAGA	GGTGGAGGGA-AGAG	CCCGATGAACC	CGGCAACCTGTCCT
Tt02	TTAAATCTCTATCAAGAGA	GGTGGAGGGA-CTGG	CCCGATGAACC	CGGCAACAGCC
Tt03	CTCAATCCCTCTATCAAGAGT	GGTGGAGGGA-CTGG	CCCGATGAACC	CGGCAACGGGCAC
Ft01	TGAAATTAACCATCAAGAG	AGATGAGGGA-CAGG	CCCGTTGAGATCT	CAGCAACCTACG
Ft02	AAATAATTAACCATCAAGAG	AAACGAGGGA-CTGG	CCCAATGATGTT	CAGCAACCTAC
Dt01	AGGTCACCTTTATCCAGAGT	CGGCGAGGGA-CTGG	CCCATGACCGCG	CAGCAACGGCC
Dt02	CGGTGGGGTCAATCCAGAGT	CGCCCAAGGTTG	CCCGCTACGGCG	CAGCAACGGCC
Xa01	CTTAGCCTCACCATCGAGAG	CGGCGAGGGA-CAGG	CCCTTTGATGCG	GGGCAGCAGCGGAGCG
Xc01	CGTAGCCTCACCATCGAGAG	CGGCGAGGGA-CAGG	CCCTTTGATGCG	GGGCAGCAGCGGAGCG
Se01	TTACCTAACCTTATTTGAG	AAGCTGAGGGA-TTGG	CCCATAGAAGCT	CAGCAACCGACT
Se02	ACGGATCTCTATCTCGAGT	GGTGGAGGGA-ATGG	ACCCAATGAACC	CAGCAACCTCTTT
Gs01	GTAGACCTCTATCAAGAG	TGGTGGAGGGA-AAGG	CCCTGTGAACCA	CAGCAACCGGTCCG
Gs02	ACGGCTTAACCTATCAAGAG	CGACGAGGGA-CAGG	CCCGGTGACGTGG	CGGCAACCTCCCG
Ba01	ACACATACCTCTATCAAGAGT	GGCGAGGGA-CTGG	CCCGATGATGC	CGGCAACCGAGCTATG
Ba02	AGCAATTTACTATCCAGAG	AGGTAGAGGGA-CTGG	CCCTATGACACT	CAGCAGGGGTTC
Ba03	TTTACTCATCTATCAAGAG	AGGTGGAGGGA-CTGG	CCCTTTGAACCT	CGGCAGCAGGTTC
Ba04	CGATACATCTATCCAGAG	AGGTGGAGGGA-CTGG	CCCTAGCATACCT	CAGCAACGGGT
Ba05	GAATAATCTTATCAAGAGA	GGCAGAGGGA-CGG	CCCTTTGAAGCC	CAGCAACCTCAGTTT
Ba06	AATACAAGCTTATCAAGAGA	AGCGAGGGA-CTGG	CCCGGGAAGCT	CGGCAACCTGCTT
Ba07	TGAACCTCTTATAAGAG	AGCGGAGGGA-CTGG	CCCTAGCATGCT	CGGCAGGGGACTC
Ba08	AAATTAATCTTATCCAGAG	AGGTGGAGGGA-CGG	CCCTATGAACCT	CAGCAACCCCTATGT
Ba09	ATGAATACTCTATCAGAG	AGGTGGAGGGA-CTGG	CCCTATGAACCT	CGGCAGGGGATTGG
Ba10	GAATATTTCTATCCAGAGA	GGTGGAGGGA-CTGG	CCCGATGAACC	CAGCAACCGC
Ba11	TATACAACCTTATCAAGAGA	GGTGGAGGGA-TTGG	CCCGATGAAGCC	CAGCAACCGACC
Ba12	TAAATACCTCTATCAAGAGA	GGTGGAGGGA-CGAG	CCCGAGGAACC	CGGCACCGGATCTACA
Ba13	ACGAACATCTTATCTAGAG	AGGTAGAGGGA-CTGG	CCCTATGACGCT	CAGCAACCATTAAC
Ba14	AAGCAACCTCTATGAGAGC	GGTGGAGGGA-AAGG	CCCTGTGAACC	CGGCACCTTCAAC
				-GTAAATCACTTGTGAAATGGGGGTTTATGACGGGA
				-TAAT
				-ATTT
				-GAAAT

**FIG. 41-10**



Ba15	GGATACTCTCTATCCGAGCT--GGCGGAGGGA--CAGG--CCGATGAAGCC--CAGCAACCTCACTTGTA--GTGGTAAA--
Ba16	CTGATTCTCTTATCAAGAGA--GGTGGAGGAC--TGTG--CCCTGTGAAGCC--CGGCAACCGTCAAC--TTAT--
Ba17	TTGCATAGCTTATCAAGAA--AGGTGGAGGGA--CAGG--CCCGATGAACCT--TGGCAACAGCGGT--ATA--
Bc01	CGATACATCTTATCCAGAG--AGGTGGAGGGA--CTGG--CCCTACGATACCT--CAGCAACGGGT--TTTT--
Bc02	CAACAATCTTATGTTGAG--AGTGGAGGGA--CGGG--CCCTATGAACCT--CGGCAACCTCGT--ATGAG--
Bc03	AATACAAAGCTTATCAAGAGA--AGCGGAGGGA--CTGG--CCCGGGAAGCT--CGGCAACCTGCT--ATAGA--
Bc04	TGAACCTCTTATTAAGAG--AGCGGAGGGA--CTGG--CCCTACGATGCT--CGGCAACGGACTC--GATTCA--
Bc05	AAATTAATCTTATCCAGAG--AGGTGGAGGGA--CGG--CCCTATGAACCT--CAGCAACCCCTATA--TATATT--
Bc06	ATGAATCTTATCAGAG--AGGTGGAGGGA--CTGG--CCCTATGATACCT--CGGCAACGGGATTGG--TTA--
Bc07	ATTAGTTTCTTATTAAAG--AGTGGAGGGA--CTGG--CCCGATGAATCT--CAGCAACAGGCT--ATAAA--
Bc08	GAATATTTCTTATCCAGAGA--GGTGGAGGGA--CTGG--CCCGATGAAGCC--CAGCAACCGC--GAT--
Bc09	TAAATACCTCTTATCAAGAGA--GGTGGAGGGA--CGAG--CCCGACGAACCT--CGGCAACCGATCTAC--AATT--
Bc10	AGACAACTCTTATGAGAG--GGTGGAGGGA--AAGG--CCCTGTGAAGCC--CGGCAACCTTCAAC--GAAT--
Bc11	ACGAACATCTTATCTAGAG--AGGTAGAGGGA--CTGG--CCCTATGAGGCT--CAGCAACCATTAAC--ATTT--
Bc12	TATACACTCTTATCAAGAGA--GGTGGAGGGA--TTGG--CCCGATGAAGCC--CAGCAACCGAC--GTAAATCCATTGTGAAATGGCGTTTATTACGGC
Bc13	GGATACTCTCTATCCGAGCT--GGCGGAGGGA--CAGG--CCCGATGAAGCC--CAGCAACCTCACTTGT--ATTGGTAAAC--
Bc14	CTGATTCTCTTATCAAGAGA--GGTGGAGGGA--TGTG--CCCTGTGAAGCC--CGGCAACCGTCAAC--TTTAT--
Bc15	TTGCATAGCTTATCAAGAA--AGGTGGAGGGA--CAGG--CCCGATGAACCT--TGGCAACAGCGGT--ATA--
Bc16	TTTACTCATTTGATCAAGAG--AGGTGGAGGGA--CTGG--CCCTTGAACCT--CGGCAACAGGTTCA--TTTT--
Bc17	ACACATCTCTTATCAAGAGT--GGCGGAGGGA--CTGG--CCCGATGATGCC--CGGCAACCGAGCTTATA--ACG--
Bc18	AGCAATTTACTTATCCAGAG--AGGTAGAGGGA--CTGG--CCCTATGACACCT--CAGCAACGGGTTCT--GTAATA--

FIG.41-11

Cons	<-----P3-----<PS- .....r.GTGYaa.t-Cc.r	---P4--> carr.....	<-P4---<-----*-P1-- .....yytgrraGATRagrr.rr.....
Bs01	GCATGACCAAGGTGCTAAAT-CCAG	CAAGCT	CGAACA
Bs02	GCAAGGCGCAAGGTGCTAAAT-CCAG	CAAGCGT	TTTTT
Bs03	TGATGTCTCATAA	CAGAT	TGT
Bs04	GCTGTCTCTTAA	T	CTG
Bs05	AAGCAGCGTGCTAATT-CTTG	CAGCT	AGC
Bs06	TGTAAAGGTGCT-ACCTCCAG	CAAAATG	AATTC
Bs07	IGTGCCCAATT-CCAG	CAAGC	GCTA
Bs08	GAGACAACCAAGGTGCTAA-CCTG	TTGCAAGG	TTGTATGATT
Bs09	GTTGAATGGTGCCCAATT-CACA	CGAAGC	GTTC
Bs10	AACAGAAATGGTGCTAAAT-CCCT	AAGAAC	ATTG
Bs11	ACAGAAATGGTGCTAAAT-CCCT	TAGACAA	TGA
Bh01	AAAGAGGTGCCCAATT-CCAG	CAGAACA	TGA
Bh02	AGCAACGAGGTGCTAATT-TCAG	CAGAAATG	ATTT
Bh03	IGTGGTCAGGTGCTAATT-CCCTG	CAAGCA	TTAAT
Bh04	AGGTGAAGAGGTGCTAA-CCCTG	CAAGCC	GTT
Bh05	GCTTGGAAAGGTGCTAATT-CCCTG	CAAGCC	GAT
Oi01	AGGTATGGTGCTAATT-CCAA	TAGGCT	TACA
Oi02	TAAGTACGTGGCCCAATT-CCAG	TAGCG	TAAT
Oi03	TCGTGCTAAAT-CCCTG	CAAGC	AATA
Oi04	GGAGTGGTGCT-TCCTCCTG	CAGAA	TTTT
Oi05	GGTGAAGAGGTGCTAA-TCCTG	ATGCAAGGA	TAATAGT
Oi06	ATGAAGAGGTGCCCAATT-CCCTG	CA	GAAA
Oi07	AGAATACGTGGCCCAATT-CCAT	CAAGCA	AAT
Oi10	GAATACGTGGCCCAATT-CCAT	CAAGTAT	TCT
Oi08	GTAACATGGTGCTCATT-CCAG	CAAGC	GTAG
Oi09	GCTATGAAGAGGTGCTAAAT-CCCTA	CAGAC	TTATC
Oi10	GAATACGTGGCCCAATT-CCAT	CAAGTAT	TCT
Oi11	TAGAAGGTGCTACCT-CCAG	CAAGAT	GTAT
			GTCTTGAAGATAAGAGTCCAGATTAAAAAAA

FIG. 41-12

0i12	-----TAAAGNACTGTGCCAATT-CCCTG-----CAATGCG-----AAACGA-----GCATTGAAAGATGAGAAAGCATGCTTCTACATATATACATATG
0i13	-----GTGATGAATAGGTGCTAAAT-CCCTG-----CAAAATAC-----GGACA-----GTATTITGAGAAATAAGAGAGGTGATGAATGACTTACGTAGTGTA
Ca01	-----TTGGAGATGTGCTAATT-CCCTA-----CAGG-----TTTAT-----CCTGAGAGATGAGAAATGTTTTTAAAA-----
Ca02	-----AATATATGGTGCTAAAT-CCCTG-----CAGC-----AAAC-----GCTGATAGATGAGAAATAATCGCGAATGTAAA-----
Ca03	-----ACTTATGGTGCTAATT-CCAG-----CAGGA-----TATT-----TTCTGAAAGATGAGGAGCGACTATTAAACATTTTTATTGT
Ca04	-----TATACAAGGTGCTAATT-CCCTG-----CAGC-----GCTA-----GCTGAGAGATGAGAAATATAAATCGAGCTTTTA-----
Ca05	-----GTACGGTGTTAATT-CCCTG-----CAAAAC-----TTATT-----GTTTTGAAAGATAAGAAACACAGCTTATTAAATGAGTATGTT
Ca06	-----AGATGATGGTGTTAATT-CCCTG-----CAAG-----TTAA-----TTTTCAGAGATAAGAGGATTATAAAATTTTAGAAAGCTAAAA-----
Ca07	-----AGTACATAATGGTGCCAATT-CCCTG-----CAGAA-----TTA-----TTCTGCAAGATAAGAGAGAGAAATGTAA-----
Cp01	-----TCACTACGGTGCCAATT-CCGG-----TAAAGA-----AAT-----TCTTTACAAGATGAGAGAAAGATAAAATTTAGTGTATAACTAAAA-----
Cp02	-----TTATAGCGGTGCTAAAT-CCCTG-----CGGT-----AGAA-----ACTGAGAGATAAGAAAGAGAGTCTGTAAAGAAATAATA-----
Lm01	-----GTTCTATGCTAATT-CCGAT-----CAGAA-----GTAATA-----TTCTGGCAGATAAGTAGTAGCTTCAATGAGG-----
Lm02	-----ATAAGTGAAGGTGCTAATT-CCAG-----CAAAATGG-----TGATT-----CCGTTTTGTTAGATAAGAGGAGCTGGATATGTTGACTTTCC-----
Lm03	-----TTTCACGGTGCTAATT-CCAG-----CAG-----TATATT-----CTGAAAGATAAGTCGSAATCCAAGTTTAGGAAACTCTAT-----
Lm04	-----TCACGGTGCCAAT-CCAG-----CAG-----GTAACA-----CTGACAGATAAGGCACCGCAATCAGGTAATAATTACT-----
Lm05	-----GTGAAGGTGCTAA-TCCTG-----TTGCAGGAG-----TATTAT-----CTTCGACGATGAGAGGCAAGGTATAATTAT-----
Lm06	-----TTGAAAAGGTGCTAAAT-CCCTG-----CGAAGTG-----TGA-----TGCTTOSAGAGATAAGAGAGACTTAAAAAGTTTCAGTGTATTGT
Lm07	-----TTATGTTTTAAGGTGCTAAGT-CATG-----CAGAACAA-----CTAA-----TTGTTCTGAAAGATGAGAGAGGAAAGTTAGTCCATTTGAAAAAATGCT
Li01	-----GTTCTATGCTAATT-CCGA-----T-----CAGAA-----GTAATA-----TTCTGGCAGATAAGTAGTAGCTTTAATGAGG-----
Li02	-----GTAAAGTGAAGGTGCTAATT-CCAG-----CAAAATGG-----TGATT-----CCGTTTTGTTAGATAAGAGGAGCTGGATATGTTGACTTTCCA-----
Li03	-----TTACCGGTGCTAATT-CCAG-----CAG-----TATATT-----CTGAAAGATAAGTCGSAATCCAAGTTTAGGAAACTCTAT-----
Li04	-----TCACGGTGCCAAT-CCAG-----CAGT-----ATC-----ACTGACAGATAAGGCACCGCAACAGGTAAATCACT-----
Li05	-----GTGAAGGTGCTAA-TCCTG-----TTGCAGGAG-----TAATAT-----CTCTGACGATGAGAGCAAAAGGTATAATTATA-----
Li06	-----TTGAAAAGGTGCTAAT-CCCTG-----CGAAGTG-----TGA-----TGCTTOSAGAGATAAGAGAGACTTAAAAAGTTTCAGTGTATTGT
Li07	-----TTATGTTTTAAGGTGCTAAGT-CATG-----CAGAACAA-----CGAT-----TTGTTCTGAAAGATGAGAGGAAAGTTAGCCCATTTGAAAAAATGCT
Sa01	-----AGCACGGTGCTAAAA-CCAA-----CGAG-----TTA-----CTCGAATGATAAGTATAAAGA-----
Sa02	-----GAAATGGTGCCAATT-CACA-----TAAAGT-----TTA-----ACTTTGAAGATGAGAGAAACAATACTACTAT-----
Sa03	-----AAAAGAAAGGTGCCAAA-CCGT-----TTGCAGAC-----AAATAG-----GTCTGAACGATAAGAGCGCAATGGAGGTATTA-----
Sa04	-----ATGTGCCAATT-CCAG-----TAACCG-----TAA-----TGGTTTGAAGATAAGCAGGTAAAGCACATGAAA-----
Sc01	-----CCGGCTAGGGAAGGTGCCAAT-CCGT-----CTACGGCG-----AGATG-----CGTCGTGAGGAAGATGAGGAGAAAGGGGCTCGGCTCCATGGCTGTGC

FIG.41-13



Ba15	-----TACAGGTGAATAGGTGCTAAAA-CCTG-TG-CGAGGCT-ACA-----GGTCTCGAACGATAAGAGCGAAGGCGAAAAAGCAGTATGCAAGTA
Ba16	-----GTTGAAATGGTGCCAAAT-CCTG-CAAGC-AAATG-----CTTIGACAGATGAGAGAGGGGATAATGTTGTTATATACGCAT
Ba17	-----ACGGAAITGTGCCAAAT-CCTG-CAGG-TAATAAAT-----CCTGAGAGATAAGAAGAGCCCTTAGAGCGTGTTCCTCAA--
Bc01	-----AATACCGTGCTAACT-CCAG-CAAGCCT-ATGAA-----AGGCTTGGAAAGATGAGAAGATGTGAACGAGTACATATAA-----
Bc02	-----ACGAAAGGTGCCAAAT-CCTG-CAGGTG-AAGAAA-----CACCTGAAAGATAAGAGCGGTTCAATTAGTCAAGAAG-----
Bc03	-----AAGCAAGGTGCTAAAT-CCAG-CAAAATGG-AAT-----CCATTTTGAAGATAAGGTAAATATATATACCGAACAG-----
Bc04	-----GAGTGCTGTGCCAAAT-CCAG-CAAGC-ATAT-----GCTTGAAGATGAGAAGAGCGTTTCTTATAGATGTATAA-----
Bc05	-----TATAGGAAGGTGCTAAAT-CCG-CAGAGAACAC-GAT-----GTGTTTTTGGAAAGATAAGAGGATCTTGAACGTGAAAGAAAA-----
Bc06	-----TGAATACTGTGCCAAAT-CCAG-CAAG-GTAA-----CTTGAAGATAAAGAAAGAGCTCATTTTGAAGTGTATATGCAG
Bc07	-----AGTACTGTGCTAAGT-CCAG-CAAAGCT-ATGAA-----GCGTTTGGAAAGATGAGGGGAAATGGATTAAACATTCAA-----
Bc08	-----GCAGGTGCTAAAT-CCAG-CAGAACCA-TATT-----TGTCTGGGAGATAAAGACGAAAGATATATACGTAA-----
Bc09	-----GTAGACACGGTGCTAAAT-CTCG-CAGC-ATTAC-----GCTGACAGATAAGGAGCTGGTTGTAAAAAA-----
Bc10	-----GTTGAAACGGTGCTAAAT-CCAG-CAAAAC-GAAT-----GTTTTGCATAATAAGAGAGGAGGATCGATTATGT-----
Bc11	-----GTTAATAAGGTGCTAAAT-CCAG-CAAAAT-GTGAA-----GATTTCACAGATGAGAAGAGACTCTATTCAAACCGAAA-----
Bc12	AAAA-----GGCACGGTGCTAAAT-CCAG-CAGAAAGT-AAA-----ACTTCTGGCAGATAAAGAGGGGAGAGATAAACTTCAAA-----
Bc13	-----ACAAGTGAATAGGTGCTAAAA-CCTG-TG-CGAGGCT-ACA-----GGTCTCGAACGATAAGAGCGAAGGCGAAAGAGAGTATGCAAGTA
Bc14	-----GTTGAAATGGTGCCAAAT-CCTG-CAAGC-AAAT-----GCTTIGACAGATGAGAGAGGGGATAATGTTGTTATATACGCAC
Bc15	-----ACGGAATTGTGCCAAAT-CCTG-CAGG-TAATAAAC-----CCTGACAGATAAAGAAAGAGCCCTTAGAGCGTGTTCCTCAA--
Bc16	-----TGAATACTGTGCCACTT-CCTG-CAAGCT-TTAT-----AGCTTGAAGATAAGATGAGGAGCTTCGTTTATATAGGGGTGCA
Bc17	-----TATAGCTAAGGTGCTAAAT-CCTG-CAAAACGA-GTTC-----TCGTTTTGGAAGATAAGAGAGGAATCTATTTTGTCTATTGG-----
Bc18	-----GGAACACCGTGCTAAAT-CCAG-CAAG-CAAGT-----CTTGAAGATAAGTGTATGCGGCCCTTGTATTATAA-----

FIG.41-15



Oi12	GTACGAA	-----TCCCTCTTTCTCTG-----	TCCTT-----	-----CAAGAAAGAGGGA	TTTTTTTATTCGCTTGGGGTTGAGACATGATTGAATTCAGAAITGTAACA
Oi13	TGTTA	-----TGCTCTCGAT-----	TTAC-----	-----ATCGGAGGCA	TTTTTTAGTTCCCGAAAAATTCACAACATGAGAAAAGAGGAGATTTA
Ca01	-----	CTGCTCTTATTT-----	TTAAT-----	-----GGATAAGAGCAG	TTTTTTTATTTATAGGAGGAGAAATTAIGGAGAAAATAGATTGTA
Ca02	-----	GCCCGAGG-----	TTATTT-----	-----CCAAGGGCT	TTTTTTATTCCTATTTTTAAGGGGGCTAACTTATGAATCTTCACTA
Ca03	TAATAGA	-----TCCCTCTCTT-----	TTAA-----	-----AGAAGAGGA	TTTTTTTGTTAATAATAGAACCAACTTATTTATTTTGGTTTTATCTTA
Ca04	-----	GAGCCAGAG-----	TTTAT-----	-----CTCTGGCTC	TTATTTTTAATCTAATGGGAAAAGGTGAATGACATGATAGAAAATAA
Ca05	AATAA	-----TCCGTTTTTC-----	TTAT-----	-----GGAAAAITGA	TTTTTTTATATATTTAAATTTAACTAGGACGGTGAAAAAAAATIGCCTATA
Ca06	-----	TCCCTCTC-----	AACTAA-----	-----GAAGAGGAT	TAAATTTATATATTTTTAGGTTTAGATATTGAAGTTAAAAATATAATAA
Ca07	-----	GTCCTCTC-----	TTAT-----	-----GAGGAGAC	TTTTTTTATTTGTAGGAGGAAGTGGATATAATATGAGAAAGTTATTAC
Cp01	-----	TCCTCTTAAATCT-----	TTAA-----	-----AGGTTTGAGAAGAGA	TTTTTTTATTAAACAAAAATATTTAAAGGGCGGCATTAAAAATAAAGTTTGT
Cp02	-----	CTCTATC-----	CTAG-----	-----GATAGGAG	TTTTTTTATTTGTAGGATAAAGGATAGATTTTAAATGGATTAGGAGGA
Lm01	-----	TGCTTCGATCTG-----	ACCAAAAA-----	-----CAGAGGAAGG	TTATTTTAGCGCTTAAGAGGGGAGTTTTTGTAGATGAAGAAAATTT
Lm02	-----	ACTCTCTAT-----	CTAA-----	-----AATAGAGAAG	TTTTTTTATGCTTTCATGAATAAATCTGGAATAATCACACAACATACTAGG
Lm03	-----	CCCTCTCGCGG-----	CTTATATA-----	-----CTGCTAGGGAGG	TTTTTTGTATGAGAAATTAAGTATCAATATCAAGAGGAGTGGATTTTA
Lm04	-----	CTTCCCTTAAAG-----	CTGT-----	-----CTTTAAGGAAAG	TTTTTTTATACATAAAAAATAATAGAAATGAGCGGAAGAAAATGAACCAAG
Lm05	-----	AGCCTTCTCTATCGTGGCGTTT-----	GTGCAAAATAGAGAGGCT	TTTTTATATGAGACGTTATTTGGAGAGAAATGGAAGGAGGAAAATAAAATTTGG	
Lm06	GTATCGAAACTTCCAAA	-----CCCTCTAG-----	TTCT-----	-----CTAGGAGG	TTTTTTATTTGGCAAAAAATCGAGAGATAAGGTGATAGGTAAGGTAAGGC
Lm07	-----	GCTTCTGCT-----	CATC-----	-----AGCAGAAAGGCT	TTTTTTGTATATCAGAAATGTAGAAAAGGTGATAGAGATGATTACGTTACA
Li01	-----	CGCTTCGATCTG-----	ACCAAAAA-----	-----CAGAGGAAGG	TTATTTAGCGCTTAAGAGGGGAGTTTTTGTAGATGAAGAAAATTTTA
Li02	-----	CTTCTCTAT-----	CTA-----	-----AATAGAGAAG	TTTTTTTATTTGCTTTCATGAATAAATCTGGATAAATAATCAACATACTAGG
Li03	-----	CCCTCTCGCGG-----	CTTATATA-----	-----CTGCTAGGGAGG	TTTTTTGTATGAGAAATTAAGTATCAATATTAAGAGGAGTGGATTTTA
Li04	-----	CTTCCCTTAAAG-----	CTGT-----	-----CTTTGGGGAAAG	TTTTTTGTACATAAAAAATACTAGAAATGAGCGGAAGAAAATGAATCAAG
Li05	-----	GCTTCTCTATCGTGGCGG-ITT-----	CGTGCAAAATAGAGAGGCT	TTTTTATATGAGACGTTATTTGGAGAGAACTAAAGGAGGAAAATAAAATTTGG	
Li06	GTATCGAAACTTCCAAA	-----CCCTCTAG-----	TTCT-----	-----CTAGGAGG	TTTTTTATTTGGCAAAAAATGAGAGGATAAGGTGATAGGTAAGGTAAGGC
Li07	-----	GCTTCTGCT-----	CATT-----	-----AGCAGGAAGGCT	TTTTTTGTATATCAGAAATGTAGAAAAGGTGATAGAGATGATTACGTTACAG
Sa01	-----	CTCTTACTTT-----	TCAAT-----	-----AGGGTGAGAAG	TTTTTTTGTATGAGGAAAGAACAAATGACAAAATACACAGTAGATACTT
Sa02	-----	TGCTTCTCAATTT-----	TCTATC-----	-----GATATTGAGAAAGCA	TTTTTTTATTTAAGCAACACAGGGAGGAAATCAACGTGATTGAATTA
Sa03	-----	GGCTTCTCTCTAT-----	ATTA-----	-----ATAGTTAGAAGG	TTTTTTTATTTAGTCCACAGAGAGAGAAATTTTCGTAATATAAATTTAAAGGA
Sa04	-----	ACCCTCTCTTCA-----	TCGTT-----	-----TGTGAGAAAGAGG	TTTTTTTAAATTTGGAAGCAGGTAAAAAGGATGGAAGTACATAAAAAAGAGCA
Sc01	AGACTGCCGAACCTCCAGAAC	-----	-----	-----CCACGACGCGCGCGT	CGACCTCGGCCCGCCCGCTGAGCTGCCGGG

FIG.41-17



Cons	-----T-----> -----T-----<-----T----- .yyyyy.....rrrrr.tttty.....
Ct01	CTTGATGCTCCGGCACATACCTCTGACCCGACGGCGACTAGGATCGAGGCTTCAACCTTGTTACCATTTGCCATGAGTGAGGATAACACCTTCGGTTCGAGACCTTGCAGGTTCAC
Tt01	-----CCTCTTCT-----TTT-----AGAAGGGTTTATTTTGCTCTTAAGGAGGAAGAAGATGCGTAGACTCTTTACTTCTG
Tt02	-----GTCTCTTC-----TTTTAGC-----GAAGGGACTTTTTTATTTTTAAAAAGGAGGGGCAITAAATGTTGAAAAATGAAAGCT
Tt03	-----TTACTAGGCCCTCTTC-----TCATT-----GAAGAGGCCCTAAGAAATTTCTGGAGGTGCAAAATGAGGGTAAGATTGGGTGATGGGACTTGGA
Ft01	-----CTCTAICT-----GGAATT-----GGATAGAGTTTTTATTTAATATTTTGTAAATTTTTAAGGAGGGAATAATGAAAA
Ft02	-----TCCATACT-----CTATAA-----GGTATGGATTTTTTAATTAAAGTAAGAAATTTATTATAGAAAGTAGGGATATAAATGATTAA
Dt01	-----TGGCGTCCCTTCCAGACTTCTTTTGGTCCAGGAAGGGGAGCCCGTTTGGGCGGACCTCTCGCTCTCCCAACGGAGGCCCGCCCGTGACCTT
Dt02	-----CATCACCCAGAGGGTGGCTTCC-----GCCAATCCGTCCATCAACCATCAACCGTCCACCATCACCGAGGCCGCCCGC
Xa01	-----GAGCTCC-----GOGAAGCTCGATGGCC-----GATCCACCTCGATACCGCAITGAGCCCTGTAATCTGCATGCGCGTCTA
Xc01	-----GAGCTCCCGCGAAGCTCGATGGCC-----GATCCACCCCGGATATCGCAITGAGCCCTGTAACACAGCATGCGCACTCA
Se01	-----GTGCCTTTACATC-----ATTT-----GAGTAAGGCACTTTTTAGTTGAAGGAGGTAGGAACATATTATGACGAAATTACACGGTTAATA
Se02	-----TATCTATA-----
Gs01	-----GGCCCTTCCCG-----TTTCC-----CGGAGGGGGCTTTTCATTTTGGCGCGCGCGACGCGCCGTGGGAATCATGTCCGTGG
Gs02	-----TCTCTTCCG-----CACCC-----CGGAAGGGGATTTTTCATTGTGAGGAACCATGAACATCGCGACGAGGACAGATC
Ba01	-----GCACCTCTC-----TTATTTT-----GAGAGGTGCTTTTATTTTGGAAACATATAGAAGGGGAACTATAGATGAAAAAGTATT
Ba02	-----GCCTTGATCTTA-----TTTTT-----TAGGATCAAGGCTTTTGTATCTAAAAAGAAAAAGGGAGTAATGGAAGAAAGTACGTTTATA
Ba03	-----TCCCTCTTCTC-----AATAC-----GAAAAGAGGATTTTTTATTTTTCATTTCCCTCATCATCATCCAACCTTAATTTATTTAGGAG
Ba04	-----GTGCTCTCTCTTATC-----TTTATGGTT-----GATAAGAGGAGAGCACTTTTTATTTTACCTGAGAGCTCTACTTCAAGTTTTTACAGCATATAGGAG
Ba05	-----CTCATCTTC-----TTGATCAT-----GAAAGGTGAGTTTTTATATTTTCAAAACATATATGAGGTATTTAAAAATGAAAGTAAIT
Ba06	-----TCTTTTC-----GAAATG-----GAAAGATTTTTTTTATGAAATAAAAAGGGGGCTGTTCCGCTGAGCGTACGGGAACAT
Ba07	-----GACCTCTTCT-----CGTT-----GGAAGAGGTCCTTTGTTATTCATTAGAAAAAGGTTGAAACTAGGGAGAGATGGTACTTTTG
Ba08	-----TGACCTCTT-----ATGT-----AAGAGGTCATTTTTTGTTGATAGAAAGGGAGTGTGATGCTAATTCATTTTCAAAATA
Ba09	-----GCCCTCTTCTA-----TCTTT-----TAGAAAGAGGCTTTTTTACGTGAAAAATAAAGGAGGAAGAAAAATGGGAGGCACAGGAGTAG
Ba10	-----CTTCTTC-----TTATC-----GGAGAGGTTTTTTTATTCGAAAAAACCGATTACGAAAAAATTTATATTAAAGAAAA
Ba11	-----CCCTCTTCT-----TAGT-----GGAAGAGGTTTTTCTACGTGCAAAAAACCTCTGAATGAAAAAGGGGGAGAGACGATG
Ba12	-----CCCTCTC-----CTTAGCT-----GAGAGGTTTTTTTATTTAACTAGGAGTTATAACAAATGAGCGGAATTTATAGCGACGT
Ba13	-----GCCTTCT-----TCTT-----GAAGGCTTTTTTATTTTATTTCACTACTGTTCAATTTAAAAAGGAGGAATTTT
Ba14	-----CCCTCTTCA-----AAG-----TGAAGAGGGGGTTTTTATATGATAGAAATGAGGAGATTTTGTGAAATTTACTAGATTTATTG

FIG. 41-18



Ba15	GCAAAATTAAA	-----	CTTTCCTCT	-----	ATATAA	-----	AGTAGGAAAGGTTTTCTGTATGCTTGTGTGGGAGAAATAAATGATATGTGCGCAATCTGTGGCA
Ba16	ATAAA	-----	CCTTCCTGCTT	-----	CTCTA	-----	AAGCGGAAAGGTTTTTGTGTTGAATGTGGAGGACATTCAAATAATAAAAGTAATGAGA
Ba17	-----	-----	CTGCCTCTCTCTG	-----	TTTT	-----	CAGGAAGCGGCGAGTTTTTATTTGTATATAAAGAAAGGAGAAATGAGAAATGGGAGAAATCATGGG
Bc01	-----	-----	GTGCTCTCTCTCTTAATC	-----	TTTATGGTT	-----	GATAGAAGAGGAGGACATTTTATTTACCTCGAGAGCTCTGCTCAAGTTTTACACAGCATATAGGAG
Bc02	-----	-----	GCTACTCTTAAT	-----	TTGG	-----	ATAAGAGTAGCTTTTTTATTTATGGCTAAAGTTAAAGGGGAAATAGGTAGTGGAGTATGGTTTT
Bc03	-----	-----	TCTTTTC	-----	GAATG	-----	GGAAAGATTTTTTTATGAATAAAAGGGGGCTGTCGCGTAGCGTAGCGGGAACAT
Bc04	-----	-----	GACCTCTCT	-----	CGAT	-----	GGAAAGAGGCTTTTTGTATTCATTAGAAAAAGGTTGAAACTAGGGAGAGATGGTACTTTGA
Bc05	-----	-----	TGACCTCTT	-----	ATGT	-----	AAGAGGTCATTTTTGTGTATAGAAAGGAGTGTGATGCATAATTCATTTTCAAAATA
Bc06	AA	-----	GCTCTCTCTA	-----	TCITT	-----	IAGAAAGAGGCTTTTTATGTGAAAAATAGGGGGAAGAAAAATGGAGCGACAGGAGTAA
Bc07	-----	-----	CTCTCTTAAT	-----	ATGT	-----	GTAAAGAGAGTTTTTATTTAGAGAGGGGGATAGAGTGAAGTTTGATGTAACGTATTTTT
Bc08	-----	-----	CTCTCTC	-----	TTATC	-----	GGAGAGGTTTTTTTATTTGCAAAAAAACCGATTACGAAAAATTTATATTAGAAGAAAAAGG
Bc09	-----	-----	CCCTCTC	-----	CTTAGCT	-----	GAGAGGTTTTTTTATTTAACTAGGAGGTATAACAATGAGCGGAATTTATAGCGACAT
Bc10	-----	-----	CGCCCTCTCA	-----	AAG	-----	TGAAGAGGGGGTTTTTATATATGATAGAAATGAGGGAGATTTGTGAAATTTACTAGATTTATTA
Bc11	-----	-----	GCTCTCT	-----	TCIT	-----	AGAAGGTTTTTTTATTTTATTTCAACTAATGGTTCAATTTAAAGAGGGAATTTTC
Bc12	-----	-----	CCCTCTCT	-----	TAGT	-----	GGAAAGAGGTTTTTCTACGTCAGAAAAACCTCTGAATATAAAAAAGGGGGAGAGACGAT
Bc13	GCAAAATTAAA	-----	CTTTCCCT	-----	CTCTATTATGT	-----	AGGAAAGGTTTTTCTGATGCTTGTGTGGGAGAAATAATGTATGTGCGCAATCTGTGGCA
Bc14	ATAAA	-----	CCCTCTGCTT	-----	CTCTA	-----	AGGCAGAAAGGTTTTTGTGTTGATGTGGAGGACATTCAAATAATAAAAGTAGTGATA
Bc15	-----	-----	CTGCTCTCTCTCTG	-----	TTTT	-----	CAGGAAAGGGCGAGTTTTTATTTGTATATAAAGAAAGGAGAAATAAGAGATGGGAGAAATCATGGG
Bc16	TAACTGTACGTAAAAA	-----	TCCCTCTCTC	-----	TCATAAT	-----	GAAAGAGGGAATTTTATTTTATTTTCAATTTCCCTCATCATCCAACTTAATTTATTAGGAG
Bc17	-----	-----	GCACCTCTC	-----	TTATTTTT	-----	GAGAGGTGCTTTTTTATTTTGGACGTATATTTAGGGGGGAATTTAGATGAAGAAAGTAT
Bc18	-----	-----	GCCTTGATCTTA	-----	TTTTT	-----	TAGATCAAGGCCTTTTGTATTTCTAAAGAGAGAAAGGGAGTAAATGGAAAAAGTAGCTTCATA

FIG.41-19

Cons	.....
Bs01	GGGACATTTAGAAAGATTGCAAGACAGGTGTTAATCGGTGACGGGCCCATGGGACGCTCTCTACTCTATGGCATTGACAGGTGTTTGAGGAGCTCAATATTTCAAAGCCGGAGGA
Bs02	CGAAATTAGCTCAAAATTTGGGAACCGTAGCGATGAAGTACGGGAACAGTGAAGTCTCTATCTATTTATCAACAGCATACCGCCACAGAGGATCGGAGAACTACCGGATTTGATTATG
Bs03	GTGTTTACATATAAGGAGGAGAAACAATGACACACCATCAAAACATCGAATTTAGGATTTCCGAGATCGACCTGAACCGGGAATGGAAAAAGCACATTGAAGCGTATTGGAAAAAGGCAG
Bs04	GGAGTCAAAAACACCTTTATACGAAGCTTAAATGAAGCTCGGTGGCGTGAAGCTTGGCTATTTCCAGCAAAAGCAGCGTGACATGCCAGGAGATCGGAGAGCGGC
Bs05	GGGACATATCTCTGACCGAACCGGAGCCGATACAGAGAAGAACAAATCGCAACAGGATTGACAGTAGGCTCTGGACTGATCTGCCCTTGTAAACAGGAGCAAAATGCAA
Bs06	CACATTTACATGGGAAAAGACACCGGCAGAAAGCTACTGTTTGTGTCTCGAAAGGAGGAAAGAAATGTTAAGTATGATAATTTGGGAAGAACCAACGATTACATTTCCGGAAGA
Bs07	TGGTTACAGCACCGTACAAACGAAGAGGAGCAAAAGAGCTTGAACACTTGTTTGGCTCAGTTGCTTATCAATCTTGAAGGAACAAGGTAGGGCATATCGGGAGGATGAACCTCATTCAGC
Bs08	TTGTTAAGAGGAGCGAGTTCGTATCATATATACAGGCTTTTGGGAGGCCCTTGTGAGGAGGAAGCAAAATCATGAGTAAAAATCGTCGTTTATTTACATCAGAACTCTGTTACGGAG
Bs09	GTGATTGCTTTTGATCAATCTTCAGGATGTTTCAAAGTTTACAAGTCGAACATGGAGATGTCAATGCTGTCCTCAAAAGCTTCGCTTCCATTTAAAAAGGTGAGATTTTGGAAATTAIA
Bs10	ACGAATGTTGCGGACAAAAACAGAAAAACAGCAACGCCCTTCGCGCCGATCATGTGGCAGCTTGGCTCGCTTCGGTTAAGGAAGCCGGCAAAAAAGCGCGCTGGT
Bs11	ACACCGCAGAACAAAAATCACTTCAAAGAAAAAACCGCGTTTGGCGGGATCAAGTCGGAAGCTGCTAAGATCTGAGCCGCTCAAAAAAGCGCGCTGCAAAAAAGCGCGCGGAA
Bh01	CGAAAAACAGCAAGACAAAAAAGAACAACTTGGAAATGAGGAGGGTGTGATGAAAAAATTTAGCTAATCCACGAAAAACGATGAATGGACGGTTCACTTATTTAAACGACTTGAGGA
Bh02	AAGGGAAATTAATCAGATGATTAAGTTGGTGATCGGATTTGGCACCGTTGGCAAGGTGTGTCGAGAGTCTAGTTCAATTTGGAGCGAGGATTAAGSAAAGAAAGTTACTCTCGAAT
Bh03	TGAAGGCTTCGCAACTTGGCAGCAGCTGATTTTCCAAATAGATGGATAGGAGGACCACTGAATCGTAAAGAAATTAGAAACAGCTTAGTACAAATCGGAAATCGAATGGATGATC
Bh04	ATCATGTTTGGCGAGCCTGCCGTGGTAAGGGTGCTTAAGGAGGATATTCGTAATGGCAGATACAAGAGTCTGCGCTTATTTACATCAGAGTCTGTACAGAAGGACATCTCTGA
Bh05	TAATGATTTGCGTGCTCTTGACGCAAAATTTGGCAGAGTGAGAGTTTGTCTCGTACTGACTTTTGGTTAAATTTGGTAACGGTAGACGAACTGATATATTTTAGAAAAGAGGCGCTT
0i01	GACGTTTGCAAGAAGCGGTAATAGCAGGAGAGGGGTATTTATTTGAATTAGAGAGGAGGGGTACTTACAGGCAAGTTCGTTTGTACCAAGTAGCCCTTGAAAAATCCGGATGGGT
0i02	GAGCAAGACCCCTACTCTATAAGACTAGCCCAAAATCTAAAGGAGAAAGAGGAAATTAACATGACAAAAACAGTTATTAAGCACCATTTCGGCAGACCATGTAGGTAGCTTACTACGAC
0i03	ACAAAGAAGAAATGATCTAAATTGAGAAATTAATTGCATCTAATCAATTTAAAAAGGGAAACAACATCTATATGAACCTGACACAGCAGAGTTGGAAATAGCAATACTTTAAATTAACAATA
0i04	CACATGAATCTAAAAAGAGAGAGTATAGGGGTAGATCAAGTTTCCCTTGATATCAAAAGGGAGAAATATATGGCATCGTTGGATATAGCGGTGCAGGTAAAGTACGCTTTTAGGT
0i05	TCCTTTATTGGCCTTTTGAATAGGATAGAGTTATAAGAGATCGGTACCAACATATATCAAGSAGAGTTTAGCCCTTAGCGCTGCAAAATCGAGCTTATTTACTTCAGAGTCAGTAACT
0i06	TAAGAGGAGGAATAAAGATTGATATCCATCGAAGGGTTAAGTAAGTATTTTTCATTTAAATAAAAAAGACATCAAAAGCTGATAGCTCATTGACCCCTCAATATTTGAAAATGGCGATATTTAT
0i07	TAAAAACACGCAATCTCTATTTTGTATCATTTTAAACCCTAAACCAACAAAAAGGAGATGGTGCAATTTGAATTTCTAACATAACATTTACCTGGGTTGGAAGAAGGAAATATA
0i10	CTGGTTGCCGATTTTGGAGGGTGGTTGGCTAATGTAGAAGATGAACAGATGCCCTACTTTTGAATATGCAAAACAGGTAAATTCAGCAGCGGAAGAAATGGGGATATGATACGACTTT
0i08	CTTCAAAATATGAGTAACCAATCAGTAACTAAGTAGGGGGATCGAACTGTCAAGTGATCGTAGTTTATAAAAAATCTAAATTAAGAGGAGAGCGGTGTATTTATGCCAACTATAAAAC
0i09	ACACGATGCTAAATTTCAATCTTTGCAAGCAGAAACAATCTTACTTTCAGGAGCAGGAACCCAGACCCCACTCAACTGGTTACGTTGCGAGTTCCAAATTTATCAAACTACGCTCTATGTT
0i10	CTGGTTGCCGATTTTGGAGGGTGGTTGGCTAATGTAGAAGATGAACAGATGCCCTACTTTTGAATATGCAAAACAGGTAAATTCAGCAGCGGAAGAAATGGGGATATGATACGACTTT
0i11	TGTGACATTTGCGGACGCCCTCCGAACATATCTATAGATCTGAAAAAGTACTACATTTATTTAGGGAAATCAATTAAGTGAACAGAAATTTCTATGTGACCCCATATTTCTGTAAAGATGTACC

FIG.41-20

0i12 AAGACATTCACAC TAGGAAAAGAAAGTAGAAGCTGTTAAAGAAGTATCTCTAACGATCGAAAAGGAGATATTTATGGAATATTGGGTTACGGGTGACGAGAAAAGTACCTTGCTT  
0i13 IGTCCACATCGATTGTAAAGAGAGCTCCGGGTCAATTATCGGATTGGCGGGATGTCCTGTACTGCTTGAAGAAGTGTAGTAAATGTTATACAAAGTATACGAGGGA  
Ca01 GAAATTTTGACACAAAAGCAGTTCATGGGGAGAGTGGTTTGAGAGCAGAACTGGGGCAATAGCTACCAATATACCAAGTCTTACCTTTAGACATGAAGGCTTAAATAAGGGAACCTG  
Ca02 AAGAAATTTGTTAAATAACAAAATTTAGTTTATAGTGGTGTATGGGAACATGTTCAATCCCTTAACTTAGTAGAAGCGGACCTTAAAGGTTCTTATCTTGATCATGTCATTCCAAT  
Ca03 TTAAGAGTGGTGTATAGACATATTTTAAAGAGAGAGAAATACCTCCAAATATTTCTCCCTCAATCCATAAGCTTATAGATTTACCCAATCTATCTTAAATAATTTTACTA  
Ca04 AAATGTTTCTAAATATTTTCAGGAAAAGTCTTAAAGATGTTGATCTGAAGATTAAGGGCGGAGAAATATTTGGAATTTGGTCATAGTGGAGCTGGAAGTCAACATTACTTAG  
Ca05 AAAATACCTGATAATCTCCAGCAGCAAAAACCTTAAATGAAGAAAATATATTTTATGGATGAGGATAGAGCCTATCATCAAGATATAAGACCTCTTAATATTGTTATAGTTAACCTT  
Ca06 AAGGGGATTTTAAAAATGAGTGAAGAAAGAAAATTTGGTTTGAACATACAGGTTCAATGACGACAAAGTTGCTGATCCAACTACAGGATCAAGAGCTGTAACCTATTTATCAAAACA  
Ca07 ATCTGAATCAGTAACAGAAAGGCTCCAGATAAAATCTGCGATCAATATCAGAGGCTATTTAGATGCCATATTTGGAAAAAGATCCAAATGGAAGAGTGTCTTGTAAGAACACAGTGAC  
Cp01 TAATTAAGCTTTAAAGATATTTTGAATCGTGGGAAGATAAATTAAGTTATTTGTTTAAATAAACAGGGTGGAAATAAATAAAATGAAGGGGTGAATTAGCTATCTTATATGATA  
Cp02 GAGAAAATGAAAAAAGGAAAGTTTCAGCATTAATTAATATTTTGTATCGATTTATTTGGSACTTCATTAGTAATGAAGAATTTCTACTCTGTATCTGTTTAGTTCACGGA  
Lm01 TATTAGTAGCGGTTATCTCGGTTTTCGCTTGGTGTAAACGGCTTGGGAGGTTCTGGCGTAGTTAGACAAAAGCAACCGTTACAGCAAAAGCAACCGTTACAGCAAAAGCAACCGGCTCTCTTATTATCG  
Lm02 GAGGAAAAAGATGAAAAAATTAACAAAAGGGTAGGAAATTTTAC TTGCATCAAGCTTGTTTAGGATTAGCAGCATGTTGGAGGAGGAGTGAAGTAAAGGCTTAAGCACAGAAAAA  
Lm03 TGAGTAATGAGTATAAATCGAAACAAATCAAGTACAGCGCGGACACACCCGACGGAGATACACATCTAGAGCGGTACCTATTTATCAAGGACGTCATACACATTTGATAGCCCGG  
Lm04 TAGCTCCATTTATGCGATCATGTTGGGAAGTATTTAGCGACAAAGGGAATTAAGAGCCAGAGAGAAATCCAAAGTGGCGAAATACAGCTTAGAGTTGGCAAAATCGAAAAATA  
Lm05 CTAAGAACCGTCACTATTTACATCAGATCGGTTCTGTAGACATCCAGATAAATTTGCAGATCAAAATCTGATGCAATTTAGATGCAATTTTCAAAAGATCCGACGCGCGGTG  
Lm06 GATTAGTTCAAAC TTGGGTAATCGAGACTTGGGAGAAACGTGAATGGAACGTGGTTAGAAAAATTC TGGAAATGGTGGATTTTCGGAAGAGGAATTTGTTGGCTGAACGGAAGGCTCT  
Lm07 AAACGTTGTAAAAGAATACAGTCCAGAAACAAACAAAGTTCTCGCAGTCGATCAATGTCGATTTAGAAAATGAACAAGGCGAGATTTTCGGAGTTGTAGGTTATTCGGAGCTGGTAAAAG  
Li01 TTAGTAGCGGTTATCTCGGTTTTCGCTTGGTTTAAAGGCTTGGGAGGCTCTGGCGCTAGTTAGACAAAAGCAACCGGTTACGGCAAAAGCAAGAGCGGCGCTCTCTAAATTTATCGGT  
Li02 GAGGAAAAAAGATGAGAAAATTAACAAAAGGTTAGGAATTTACTTGCATCAAGCTTATCTAGGTTAGCAGCATGTTGGAGGCGGAAGTGAAGTAAAGCTTAAGCACAAAAAGAA  
Li03 TGAGTAATGAGTATAAATCGAAACAAATCAAGTACAGCGCGGACATACACCGGACGGAGATACGATCTAGAGCGGTACCAATTTATCAACAACATCGTATACATTTGATAGCCCGAG  
Li04 TGGCACCATTTTATGCGATCATGTTGGAAGTATTTACGGACAAGGCAATTAAGAGGACCGGAGAAATCCAAAGTGGCGGAATTCAACTCAAGAAATACGTGAATTTGAATAATG  
Li05 CTAAAAACCGTCACTATTTACATCGGAATCGGTTTCTGATGACATCCAGATAAATTTGCAGATCAAAATCTGATGCAATTTTGAATGCAATTTTCAAAAGATCCGGACGCAAGCTG  
Li06 GATTAGTTCAAAC TTGGGTTATCCGAGACTTGGGGAGAAACGTGAATGSAACGTGGCGCTAGAAAAGTTTGGAAATGGTGGATTTTCAAGAGAGGAATTTATGGCGGAAACAAAAGCTCT  
Li07 AACGTCGTAAGAATATACGTCAGAAATAACAAAGTTCTCGCAGTCGACCATGTCGATTAGAAATGAACAAGGTGAGATTTTCGGAGTAGTTGGTTATTCAGGGGCTGGTAAAAGT  
Sa01 TAAATCTAGGGAATTTATACAGAAATCTGGGAAGTCATAGATAACTTCGCTTGAGATATAGCATGTTGGTTATCATGGAACAACATAGTTGTAGTTGTGTCATGCAATTAACCTGGCA  
Sa02 AGAAGTTGTTAAAGAATATCGACTAAAAATAAAGAAGTCTCTGTAGATCAGTTAATTTATCGATTGAGCAGGATCGATTTATGGCGTCAATTTGGTTTTC TGGAGCAGGAAAAAG  
Sa03 GCAAACTATGTTAAATAACAAACGATTATTTACTTCAGAGTCGTTACAGAGGACACCCAGATAAATCGCTGCAAGTGTGAGTGAATATAGATGCTATTTTAAAGAGGACCCC  
Sa04 ATGCTTGGGCATATTTCCCTTGTATTTATTTGGGCTGTTTATAGGGTAGGTTATTTATCAGAGTGAATTTTACTTCAATGCCATTAAATGTTGCAATACGATAACGTAATTTGTGG  
Sc01 AGTGGGCGCCACAGGGGTTCCGCTCGGACCGGCTCTCGGCTCGGAAGAGTGTTCGCGCCCTCGAGATCGGCTACGACTCTCGGACTACGACCGGAGAGCTGGGCAAGCGGATGGAAG

FIG.41-21

Cons	.....
Ct01	GCCTGGGACGAGCCTGTACGGGTGACGGGATGCGGCGCGTGCCCATTTACAGACCACTCTCTACGTGTTGAGAACGCGGAGCAGCGGCTGACCTGTTGCGGCTTGGCAAGGCGGGC
Tt01	AGTCAGTCACTGAAGGGCATCTGACAGATCTGTGACAGATTCAGATGCCATTTGGATGAAATTTTAAAAAAGAGCCCTTACGCCCGGTGGCATGTGAGACAGCTGTAACTACCG
Tt02	GTGTAATAACTTAAGAAAAGAAATTTGTAATACTGTGAAATTTCTCCCCCAAGGGATAGATGTAATACTAACTATCGAGAGAGCTCGAAAATTTAAAGGTGTGGCAGATGCTCT
Tt03	ACTGTTGGGACAGAGATTTAAATAGTTAATCTAGAGGAGATATACAGGAGAGTACGGGATTTATCCGGAGATAAAGAAAGTGTGTAAGGATTTGCACAAAAGAGAAAA
Fn01	GTTTACATACTTTACATCAGAAATTTGTTTCCACGAGCATCCAGATAAAATTTCCAGATCAAAATATCAGATGCAATTTAGATGCTTGTTTAAAGATGACCCCTAAATCAAGAGTTGCCTG
Fn02	CACCTGAAAATGTAAATAAAATTTAATCCATAAATTTGATGCTGTAAAAGATGTTAATTTAAAGTTAATGAAGSAGATATCTTTGGAATTTATAGGTTAAGTGGTGTGGAATATCTT
Dr01	ACCGTCTCCCCCAGCCTTGCACTTCGAAGGGGTGAGCAAAACCTACCCGGCCAGCCGGCGCGCTGAGCGATTTGACCTCACCGTTGCGCGGCGGAGCCGACCCGGCATCAT
Dr02	CAGCGATCTGTATCTGACGGCGCTTGGGTACCGAGCTTCAGCGAGCAACCTCACCGAAGCGGACTTCGGCTGGGAGAGCGGACCCACCGGATGTACCGGGGCAACTTCGAC
Xa01	CCAAGATTTGTTGACACCCCGCAGCAGCAGCGGATCACTGCGGTGCGGGGAACTTTGTATCGCCCTGCCATGCGGCATGCGGCGCATGCGGCGAGCTGCGGCTGCGCTATG
Xc01	CCACGCTGACACCTACAGCCCGCGCTGATAGCGAGCCCGCGCTGCGGTGCGGGCGAGCTGCTCAATCTACCGATGCGCCAGCGCGGCAACCGGAGCTGCGGCTGCGCTACG
Se01	CATTAGAACTAGGTGAGTTTAAAACTGAATCTGGTGAACGATTTGATCAATTTAGCTACGTTATGAACATGTAGGACTTCTTGGTCAACCCCTTGTGTTGTTGCCATGCACTTACTG
Se02	-----
Gs01	CATGTCGAAGAACAAATCCGTCACCTTCGAAGGGATCTCAGCTTGAAGCGGCGGATCTGCGGCCCATCACCTTGGCTACGAGACCTACGCGCGGCTGAACGCGGACCGGTCCAA
Gs02	GGTCTCGACTGGGATACCGGACCGGGCGGTACCGTACCAATCTACAGAGCGCAACCTTCGGGCATTCGGGATTTGGCCAGAGCAGCGGCTACGATTAATCCCGCTCCGGCAACCCC
Ba01	ATTAGCATTGTAAGCGGAGCGGTACTATTATTAGCGCATGTAGCGTGGTTCCGATAAAGAGTAAGCGTTAGATGAGAAAAGATTTACTGTGCGGTGAACAGCGGGCGCGCATGA
Ba02	AAACAAAGTAAATTCATGTGTTTAGGGGTTATGGAAGTGTATGTAATTAATAAATATCGGTTATGTTTCACTATGGGTTATTACAGAGTGACATTTCTAATTATGCAATATTAT
Ba03	GAAATCAAAATGAAAAGAAAGTTGTACCCGTTATGCAATCAGTTGTAGGAGTAAGTATTTATTAACCTGTTGCGGTAGTTATAAAACGAAGCAAGCGGAGCAAAATGCAAAAGACGAG
Ba04	GGGGAATAATGATTTCTTTAATAATGTAAGTAAGTATATGAAATCAGGTGGGCAATCTGTTCACTGCGGTGGAGGATTAAGCTTATCAGTTGAGAAAAGCGGAAATTTTGGCATTATCG
Ba05	GACCTATCACAACATTCGAAAATAATATGCTCAATTCCTGGAACCAAAATCAATTTAGAACCCATACAAGCGTTGAAGAAACAGGTTATCAAGTTACAGATTTCCATTCTGTC
Ba06	TTTGAGGAAGTCTGAGAGAAATTCAGCGGATGCTTGCTGATATGAATATGGTTCAATTTGTTGACAAGATGGAAGAGTCATCAACTAGAGAAAAGTGAAGAAAGTAAAGTAAAGTAA
Ba07	AAAGAAACGAGAGSAAATGGTTTGGCTTTATTACCACTTGGGATATTTTGGCGTATTTATAGGTTCTGGAATTTATACAGGTGATTTCTATAAAATTCGCGATACTTTAGGCAATTTCA
Ba08	AAATAGAGTAAATAAAGTTGACTATTAGAGAGGGGAAATTAATATGAACAGATTTATCAACAAAATAGTAGTAGCAATCGGAATTTGGATCAGCATTTATACGGGATTTAGGACTTTGGG
Ba09	CGTCACAAAAGAAAACAAATGAAGAGATATGAAAGAAATAAGGAAAAGTACATAGAAAACAGTCATGATATTCATCGGAATCCGGAGATTTGGTAATCAAGAAATTTACGCATCTAGAA
Ba10	GGGGTTCGGAAGTACTGTGACACTCGAAAATACGTAATAACTGGGTAGTACAGTTATGAAATATATGATAGAGCAAGATAAGCCAAATATCATTTGATATTTCAAGAACATATCGTTTC
Ba11	GGATATTATTCATTAAACAGAGTAACCGCTGTACAATATCGGAAAGAACATGGTTATTTTGAAGAAAGCAATGTAGTTTGTATGAAATTTGGAGATGGAATTTAAATATATGTTTC
Ba12	ATTTAATCCATGATGATTCACATAACTTAGAAAAAAGAGTGAAGCAATTTGACCTGGTTTAAACATTTGGCTCTTGGACTCATTTGGCCACACTTATTTGCAAGAACAGTTAAAGCAGCATA
Ba13	TACATGTCACTATCGAAACAAAACTAGCGCAAAATCGGAAACCGGAGTGAACATAACAGGAAGCTGTTAATCGCGCTGTTTACTTTTCACTGCTTATCGTCACGAAGSAAATTTGGTAAA

FIG.41-22

Ba14	TCAAAAGGAATTGTAATAGGTGATGGTGGGTGGAAACATTATTACATTACACGGTTTGCAAAGTAGTTTGAAGAAATTGAATATATCTGATCCAGATTTAATTATATCGATTTCATAAG
Ba15	AATTAAAGGATGAGTTCGGTACAATATATACAAATTACTGTAGGGAGGTTTACCACATGACAAAAACGTCATCTGTTACATCTGAGTCTGTAAGTGAAGGACATCCAGATAAAATTTGT
Ba16	ACGGTGGGCTACGGTATCAAAAAATTGCGGAGTCAATCAAAAAATTAGCTCAGCGGCTAGAACAGTCGGTCTGTTTCATCCCTTCCATAGGAGGCAAAAAAGCGGCTCTAAAGTCTG
Ba17	GGAAAGGAACGATTTGTGTCAAGGTGGCTATACGCCAAAGAAATGGAACACCGCGTGTTTACCGCTTTATCAAGCACGACGTATAAATATGATACTTCGGATGATTTAGCAGCATTAT
Bc01	GGGAAAAAATGATTTCTTTTAACAATGTAAGTAAAGTATATGAACAGGTGGCAATCTGTTCAATGCGGTGGAGATGTAACATTATCAGTTGAGAAAGGCGGAAATTTTGGCATTATCG
Bc02	TGGTTGCCGATTTTGGGGATGGCTTCGGAAATGTAATGATGAATCTATGCGGCTACGTTTGAGTATGCAAAACAAACGCGGACAGGCGGAGCAAAATTTAGGTTTTTCAACAACACTT
Bc03	TTTGAGGAGTATCTGAGAAAAATTGAAGCGATGCTTGCTGATATGAATATGGTTCAATTACAATTGTTGCAAGATGGCAAGTCAATTCAAATTAGAGAAAAAGTGAAGAAAGTACGTTTA
Bc04	AAGAAACGAGAGGAAATGGTTTGGCATTATTACCACCTTGGGATATTTTGGGCTATTATTGGTTCTGSAATTTATTACAGGTGATTTCTATAAAATTGCCGATAC TTGTAGCAATTTCAA
Bc05	AATATAGAGTAATAAAGTTGACTATTAAAGAGGGAGAAATTGTAATGAATAAAATTATCAACAAAAATTAGTAGTGGCAATCGGAAATTTGGAGCAGCATTTACGGGATATTTAGGACTTTGGG
Bc06	CGTCACAAAGAAAAACAATTGAAGAGAGTATTGAAGAAAAATTAAGGAAAAAGTACATAGAAAAACAGTCAAGTATTTTCATCGCAATCCGAGATTTGGTAACCAAGATTTTACGCATCAAGAA
Bc07	TAGAAAGTTTCCGCAATTTAAGTATGTATACATAACTTTAGGAATTACTGTAGTTTCAATGATTTCTTTTGTTATAGGATAGGTTTGGCGATCATAAACGAAAAACAAAAACGA
Bc08	GGTTGGCATTACTGTGACACTCGAAAAATACGTCAAACTGGGTAGTACAGTTTATGAATATATGATAGAGCAAGATAAGCAATATCATTTGTAGATATTCAGAACATATCGTTTCGC
Bc09	ATTTAATCCATGATTCACATAACTTAGAAAAAAGCTGAGCAAAATGCACTCGGTTAAGCAATTGGCTCTTGGACTCATTTGCCACATTTATTTGCAAGAACAAATTTAAAGCAGCATA
Bc10	TCAAAAGGAAATTGTAATAGGTGATGGTGGGCTTATTACATTACATGGTTTACAAAGTAGTTTGAAGAAATTGAATATATCTGATCCAGATTTAATTATATCGATTCATAAG
Bc11	ACATGTCAACTATCGAAACAAAAATTAGCGCAAAATCGGAAACCGGAGTGAACACTACAACAGGAAGTGAATCCACTGTTTATTTTCAACTGCTTATCGTCAGGAAGGAAATTTGGTAAAT
Bc12	GGGATATTATGCATTAACTGAACAAACAGCTATACAAATATGCGAAAGAACACGGTTTATTTGAAAGAAAGCAAAATGATTTTGTGATGAAATTTGGAGATGGAAAAATTTAAATACGTGTT
Bc13	AATTAAAGGATGAGTTCCGTACAATATATACAAATTACTGTAGGGAGGTTTACCACATGACAAAAAAGGGGTGATACACCATGATTTCTATTAGAGAAATGTAAGAAAAATATATAAGCAAAAAAGCGGTGAT
Bc14	ACGGTGGACTACACGCAATTAACATATAAAAAATTGCGGAGTCGATCCAAACAAAAAAGGGGTGATACACCATGATTTCTATTAGAGAAATGTAAGAAAAATATATAAGCAAAAAAGCGGTGAT
Bc15	GGAAAGGAACAATTTGCGTGCAGGTTGCTATACGCCAAAGAAATGGTGAACCGGCTGTTTACCGCTTTATCAAGTACAGGTATAAATAGGATACTTTCGGATGATTTAGCAGCCTTAT
Bc16	GAAAAATCAAAATGAAAAAAGTTTGTACCCGGTATTGTCATCAGTTGTAGGAGTAAGTATTTTAACTGGTTGCGGTAGTTTAAAAACGAAAGCAAGCGGAGCAAAATGCAAAAGACGAG
Bc17	TATTAAAGCATTGTAAGTGGGCTGTATTATTAAAGCGCATGTAGCGGAGTTAGATGAGAAAAAGATTTACTGTGGTGTAAACAGGAGGGGCTCATG
Bc18	AAACTAAGTAAATATATGTGTTTAGGGGGTTATTGGAGTGTATGTAAATTAAGAAATATCAGTTATGGTGTACCGCTATGGGTTATTACGAGGTTGACATTTCTAATTATGCAATATTAT

FIG.41-23

B. Cobalamin Riboswitch Alignment.

ID		Start	End	Accession	Organism
Atu01	+	70441	70625	NC_003304.1	Agrobacterium tumefaciens
Atu02	-	441331	441136	NC_003305.1	Agrobacterium tumefaciens
Atu03	+	877645	877833	NC_003304.1	Agrobacterium tumefaciens
Atu04	+	921717	921886	NC_003305.1	Agrobacterium tumefaciens
Atu05	-	1640563	1640420	NC_003304.1	Agrobacterium tumefaciens
Atu06	-	2810076	2809899	NC_003304.1	Agrobacterium tumefaciens
Bha01	-	466904	466746	NC_002570.1	Bacillus halodurans
Bha02	+	528894	529051	NC_002570.1	Bacillus halodurans
Bha03	+	870599	870748	NC_002570.1	Bacillus halodurans
Bha04	+	1661078	1661219	NC_002570.1	Bacillus halodurans
Bsu01	-	3403719	3403620	NC_000964.1	Bacillus subtilis
Bja01	+	2232813	2232975	NC_004463.1	Bradyrhizobium japonicum
Bja02	+	3617311	3617490	NC_004463.1	Bradyrhizobium japonicum
Bja03	+	3630677	3630857	NC_004463.1	Bradyrhizobium japonicum
Bja04	+	3634122	3634284	NC_004463.1	Bradyrhizobium japonicum
Bja05	-	5279669	5279495	NC_004463.1	Bradyrhizobium japonicum
Bme01	+	679030	679218	NC_003317.1	Brucella melitensis chromosome I
Bme02	+	717388	717585	NC_003317.1	Brucella melitensis chromosome I

FIG.41-24

Bme03	+	559758	559950	NC_003318.1	Brucella melitensis chromosome II
Bme04	-	973106	972933	NC_003318.1	Brucella melitensis chromosome II
Ccr01	+	502968	503156	NC_002696.2	Caulobacter crescentus
Ccr02	+	1925017	1925166	NC_002696.2	Caulobacter crescentus
Cte01	-	409802	409630	NC_002932.3	Chlorobium tepidum
Cte02	+	422045	422244	NC_002932.3	Chlorobium tepidum
Cte03	+	443769	443951	NC_002932.3	Chlorobium tepidum
Cte04	+	584183	584411	NC_002932.3	Chlorobium tepidum
Cte05	+	882576	882770	NC_002932.3	Chlorobium tepidum
Cac01	+	1509969	1510116	NC_003030.1	Clostridium acetobutylicum
Cac02	+	2557903	2558041	NC_003030.1	Clostridium acetobutylicum
Cpe01	+	248269	248429	NC_003366.1	Clostridium perfringens
Cpe02	+	1241749	1241887	NC_003366.1	Clostridium perfringens
Cpe03	-	1431291	1431152	NC_003366.1	Clostridium perfringens
Cpe04	-	1549481	1549348	NC_003366.1	Clostridium perfringens
Eco01	+	4160983	4161133	NC_000913.1	Escherichia coli
Fnu01	+	934517	934658	NC_003454.1	Fusobacterium nucleatum
Lig01	+	1347854	1347994	NC_004342.1	Leptospira interrogans chromosome I
Lmo01	+	1179829	1179979	NC_003210.1	Listeria monocytogenes
Mlo01	-	1101076	1100918	NC_002678.1	Mesorhizobium loti

FIG.41-25

Mlo02	+	1149143	1149308	NC_002678.1	Mesorhizobium loti
Mlo03	-	4044577	4044416	NC_002678.1	Mesorhizobium loti
Mlo04	-	4957334	4957164	NC_002678.1	Mesorhizobium loti
Mlo05	-	6170855	6170715	NC_002678.1	Mesorhizobium loti
Mlo06	+	6749148	6749315	NC_002678.1	Mesorhizobium loti
Mle01	-	1130394	1130222	NC_002677.1	Mycobacterium leprae
Mtu01	-	309822	309703	NC_000962.1	Mycobacterium tuberculosis
Mtu02	-	1261701	1261497	NC_000962.1	Mycobacterium tuberculosis
Pae01	+	1381520	1381688	NC_002516.1	Pseudomonas aeruginosa
Pae02	-	3261415	3261204	NC_002516.1	Pseudomonas aeruginosa
Pae03	+	3265563	3265728	NC_002516.1	Pseudomonas aeruginosa

FIG.41-26



ID		Start	End	Accession	Organism
Pae04	-	3305780	3305629	NC_002516.1	<i>Pseudomonas aeruginosa</i>
Ppu01	-	2765203	2765045	NC_002947.3	<i>Pseudomonas putida</i>
Ppu02	-	2768953	2768785	NC_002947.3	<i>Pseudomonas putida</i>
Ppu03	+	3857563	3857746	NC_002947.3	<i>Pseudomonas putida</i>
Ppu04	-	3981958	3981816	NC_002947.3	<i>Pseudomonas putida</i>
Rso01	-	2609233	2609017	NC_003295.1	<i>Ralstonia solanacearum</i>
Sne01	+	954780	954943	NC_003047.1	<i>Sinorhizobium meliloti</i>
Sne02	-	1999747	1999574	NC_003047.1	<i>Sinorhizobium meliloti</i>
Sne03	-	2122891	2122516	NC_003047.1	<i>Sinorhizobium meliloti</i>
Sne04	+	66265	66456	NC_003078.1	<i>Sinorhizobium meliloti</i> plasmid pSymb
Sne05	+	580403	580578	NC_003078.1	<i>Sinorhizobium meliloti</i> plasmid pSymb
Sco01	+	1037869	1038053	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco02	+	1045899	1046106	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco03	+	1051420	1051563	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco04	-	5688395	5688291	NC_003888.1	<i>Streptomyces coelicolor</i>
Sco05	-	6532337	6532191	NC_003888.1	<i>Streptomyces coelicolor</i>
Sfl01	+	4183416	4183566	NC_004337.1	<i>Shigella flexneri</i> (*)
Son01	+	826836	827026	NC_004347.1	<i>Shewanella oneidensis</i>

FIG.41-27

Son02	+	1071692	1071874	NC_004347.1	Shewanella oneidensis
Sti01	-	2114053	2113918	NC_003197.1	Salmonella typhimurium
Sti02	+	4347871	4348024	NC_003197.1	Salmonella typhimurium
Tma01	-	84288	84144	NC_000853.1	Thermotoga maritima
Tte01	+	395153	395353	NC_003869.1	Thermoanaerobacter tengcongensis
Tte02	+	396075	396275	NC_003869.1	Thermoanaerobacter tengcongensis (*)
Vch01	+	145142	145306	NC_002505.1	Vibrio cholerae chromosome I
Vvu01	+	1165724	1165882	NC_004459.1	Vibrio vulnificus chromosome I
Xac01	-	3631166	3630987	NC_003902.1	Xanthomonas campestris
Xax01	-	3758428	3758245	NC_003919.1	Xanthomonas citri
Ype01	-	4393235	4393008	NC_003143.1	Yersinia pestis
Aca01	-	340	170	M34485.1	Acinetobacter calcoaceticus
Avi01	-	388	214	U45329.1	Agrobacterium vitis
Bfr01	+	580	762	AY043208.1	Bacteroides fragilis
Bmg01	+	1211	1350	AJ000758.1	Bacillus megaterium
Lma01	-	76392	76234	AL499620.1	Leishmania major
Pfr01	-	543	373	AY033236.1	Propionibacterium freudenreichii
Rca01	+	105327	105521	AF010496.1	Rhodobacter capsulatus
Rca02	+	116991	117174	AF010496.1	Rhodobacter capsulatus
Rca03	-	39849	39672	AF010496.1	Rhodobacter capsulatus

FIG.41-28

Rsp01	+	201	341	B07728.1	Rhodobacter sphaeroides
Sbi01	-	330	147	BH245584.1	Sorghum bicolor
Sgi01	-	9209	9035	AF263012.1	Streptomyces griseus
Svi01	-	1235	1052	U27616.3	Stealth virus 1
Zmo01	-	24942	24808	AF193754.1	Zymomonas mobilis
Zmo02	-	4323	4162	AF193754.1	Zymomonas mobilis

Accession numbers are for Genbank sequence entries. Start and end positions are the 5' and 3' nucleotides of the first interior UG base pair of stem P1 (orange). Secondary structure (SS) and sequence consensus (Cons) lines are shown above the alignment. In the consensus sequence, uppercase and lowercase letters represent =90% and =80% conservation at a position, respectively. The degenerate bases R (A,G) and Y (C,U) appear only when a single base is not 80% conserved. Sequences marked with an asterisk (\*) were excluded when determining the sequence consensus because they have >90% identity to another sequence in the alignment.

FIG.41-29

SS	Cons	GGU	y	GGU	r	AA	GGAA	yGGU	rA
Atu01	UACUAUAUGUGGUGUUAAGGUU	UUCCGAUUC	GUUA	EGGUUGGAGU	UU	AAGACGGGAU	UCCGUGCU	UAUCCG	EGCGAFCAGG
Atu02	CCUUAUGAGACAAGCGAGGU	UCCUACAGCC	GAAA	EGCGAFCAGU	UU	AAUA	GGGAAC	AUGGUGCG	EGGGAUUC
Atu03	CGGAUAACAUUGCCGUGAGGUU	CUUUCGGG	CGU	UCCGGAAGUG	UU	AAA	GGGAAC	ACGAUAGGA	UCCUUAU
Atu04	GACAUUGGUUAGCCAUUGUGU	CUUFCGAG	GAAG	GUCCGFCAGU	UU	AAGA	GGGAU	UCCGUGA	EGGCU
Atu05	CCCAUAGCUUCGCGUAGGU	CCCGG	CUUG	EGCGGAG	UU	AAU	GGGAU	CCGUGA	AAUAUAC
Atu06	CUAAGGUAAGGACUGAGGU	CUUUCGG	GCAA	EGGGAAGU	UU	AAGA	GGGAAC	ACGUGUC	EGGCU
Bha01	AUUUAUCGUUGGGAACAGGU	ACGUUAAGU	ACAUGUA	EGCUUAAGU	UU	AAA	GGGAU	CCGUGC	AAAU
Bha02	UAGUGUUGGACGUAAGGU	CCG	CGAAG	EGGU	UU	AAA	GGGAU	CCGUGC	AAAU
Bha03	UAGCACGCUACAGCAUAGGU	GGUCAA	ACAUCCG	UUGAUGUG	UU	AAA	GGGAAG	CCGUGA	AAAU
Bha04	AUCGUUAUCCGCGUGAAGGU	CGUCAA	UGU	UUGAGCGUG	UU	AAA	GGGAAG	CCGUGA	AAAU
Bsu01	CGGAUACGAUUGUCAAUAGGU	CCCGUCCG	GAACA	ACGACCGGU	UU	AAA	GGGAAC	CCGUGA	AAAU
Bja01	CGAUUAUCCAGUGUGAGGU	CUCCGUG	CCAUU	GUCCGAGU	UU	AAGA	GGGAAG	CCGUGC	AAAU
Bja02	CAAUUGGUGCCCGCGUGUGU	CUUGUG	CUAU	EGGGAUUG	UU	AAGA	GGGAU	CCGUGA	AAAU
Bja03	GGGCACACAGGACGGCAUGU	CUUFCAGG	AAA	EGCGCGGAGU	UU	AAU	GGGAU	GGGGAU	EGGCGGAGCG
Bja04	AUCCUAGAUUGCGGACGGU	UCCUCC	GAGA	EGGGAUG	UU	AAA	GGGAU	GGGUGC	EGGCGGAGCG
Bja05	UCGUAGAUUGAUGGUGAGCGU	UUCUG	GCAC	EGGGAUG	UU	AAA	GGGAAC	GUUGGUGC	EGGGAU
Bme01	AUCGCAUUAUACGAGACGGU	UCCGCG	AUUG	EGCGGAUG	UU	AAA	GGGAAC	ACGUGA	EGGCGGAGCG
Bme02	AGUGUCAAACCAUGUGACAGU	UUUGCGG	AACGAUCC	EGCGCAUUG	UU	AAA	GGGAU	GGGAGC	EGGCGGAGCG
Bme03	GGCGUAUAACCGUACAGCGU	UCCCGAGCG	AGAG	EGGAFCAGU	UU	AAUA	GGGAAC	ACGUGA	EGGCGGAGCG
Bme04	UACCAUUAUUGUGUUGAGGU	UUUUGAUUG	GAC	EGGUGGAGU	UU	AAGA	GGGGAU	CCGUGC	EGGCGGAGCG
Ccr01	GGUGUUGCGUGUGUGUGU	CUUFCAGG	UUG	GUCCGFCAGU	UU	AAGA	GGGAAG	CCGUGC	EGGCGGAGCG
Ccr02	UAGGUUAGCUUGGUGUAGGU	UCCUG	GAAA	EGGGAUG	UU	AAA	GGGAAC	GGGUG	EGGCGGAGCG
Cte01	AUACUUAUCCGUUAUUGGU	CCCGGAG	GAAA	EGGGAUUG	UU	AAA	GGGAU	CCGUGA	EGGCGGAGCG
Cte02	GUUCUUAUCCGCAUAGAGGU	CCGGU	UAAA	AGCGGAG	UU	AAUA	GGGAAG	UACGUGA	EGGCGGAGCG
Cte03	CAUAUAUAUUAUAGUAGGU	UUCGUGCGG	GGUG	EGGCGCGGAGU	UU	AAA	GGGAAC	CCGUGA	EGGCGGAGCG
Cte04	UGAGUUAUUAUAGGUAGGU	CCGGU	GAAAG	EGGGAUUG	UU	AAUA	GGGAAG	UACGUGU	EGGCGGAGCG
Cte05	GUUCUUAUUAUAGGUAGGU	CCGGU	UAAA	AGCGGAG	UU	AAUA	GGGAAG	UACGUGA	EGGCGGAGCG

**FIG. 41-30**

Cac01	AUUGCACUA	AAA	AGGAAU	CAGGUGA	---	AAAG
Cac02	GAUAUAU	ACCUA	---	UUGGUGA	---	AAAU
Cpe01	AUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
Cpe02	AGUUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
Cpe03	AUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
Cpe04	AAUAUAUA	UUAUAU	UUAUAU	UUAUAU	---	AAAU
Eco01	CCUGUAGCAU	CCUGUAGCAU	CCUGUAGCAU	CCUGUAGCAU	---	AAAU
Fnu01	UUUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
Li g01	AUCUUGGAACG	AAAACUUGG	AAAACUUGG	AAAACUUGG	---	AAAU
Lmo01	GUUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
MI o01	CUUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
MI o02	CCUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
MI o03	AUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
MI o04	GUUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
MI o05	AGGUUUGG	CCUGUAGCAU	CCUGUAGCAU	CCUGUAGCAU	---	AAAU
MI o06	UUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
MI e01	CCACAGGCGG	CCUGUAGCAU	CCUGUAGCAU	CCUGUAGCAU	---	AAAU
Mtu01	CUUCCGUG	CCUGUAGCAU	CCUGUAGCAU	CCUGUAGCAU	---	AAAU
Mtu02	UUUUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
Pae01	AGGUUGGCGG	CCUGUAGCAU	CCUGUAGCAU	CCUGUAGCAU	---	AAAU
Pae02	GUUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU
Pae03	UUUUAUAUAU	UUAUAU	UUAUAU	UUAUAU	---	AAAU

FIG.41-31



Avi01	CCUAAAGUGGCAGCCUAUCCGU	UCUGAAUCUGU	CAAA	ACCGUCCCGAUG	AAA- GCGAAU- ACCGUGA	CGACGACCG	AAGUAA	CGGCGGAAA
Bfr01	UUUAUUUUGUCCUGAUGCGU	UCCGAAUAG	UCAUCCU	CUAU	CGCAU- AAA- GCGAAU- CCGGUGU			AAAU
Bmg01	AUCAAACAGCAACAGUAAAGGU	GGU	AAGAA	EGGU	AAUA- GCGAAA- CUGGUGA			AAGA
Lma01	-----UCCGCGUG	CCCU	UCAC	ACGGUG	AAAC- GCGAAA- CCGGUGA	CCUU	ACUUAAGGCGGUGAGU	
Pfr01	UGUGUAGGCUAGUAGUGGUGU	CGGUGGGU	CCAC	GGCAGUGG	CGCAAG- GCGAAU- CCGGUGU			AAUU
Rca01	GGCACUCAGCGCGGCGGUGGU	UCUGUG	CUAU	CACAGGUG	AACA- GCGAAU- GUGAAGGAAU	CGACGGUU	CCCCGCGAAACCGA	
Rca02	GGCUACUCCAAACAGCGGUGGU	UCCG	AACUGGAC	GGCAU- AAUA- GCGAAC- ACCGUGA	CGAAU- GCGAAC- ACCGUGA	UUUACCC	AUCA	CGGCGGUAU
Rca03	GGGCACCUUGCGCGGCGAGUGGU	CGGCGGUAACG	CAC	GGCGCGGUG	AAA- GCGAAU- ACCGUGU	CGUACUA	CGC	CGGCGGUAU
Rsp01	UGUUUUGGCGAGGCGGUGGNG	CGGCGG	UUUG	CGCGGAG	AAUC- GCGAAG- CCGGUGG			AAAU
Sbi01	UAGACUGCGCGCCACUUCAGGUG	ACUUGCGG	CAUG	CGCGAGGUG	AAAC- GG- AAC- CCGGUGA	CGGUG	AUUC	CACCGCAGG
Sgi01	UAGGUGACCGGUGGACGUGGU	CGGCGGUGG	GCCA	CGCAGGUG	CGCAAG- CCGGUGG			AAAU
Svi01	AUCCGUGGCUUACAGGAAACGGU	UCUGGGU	GAGA	GGUGGUG	AAA- GCGAAC- ACCGUGA	CGCA	UUAAAU	UGCUAUG
Zmo01	CGGAAAUUUUUUGCAUAGGU	UUCCUUUG	GAGU	CAAGGAA	AAUU- GCGAAC- AAGGUGC			AAAA
Zmo02	AGCAUAGCAAGCAUUAAGGU	CUUUGU	CAUUG	CGAAAGGU	AACA- GCGAAA- CUGGUGG	CAAA	GAAU	UUUUAAG

FIG.41-33





FIG. 41-35

Pae04	CCGCGGCTUGCCCGCCCACTUGA-ACGG	CGAUGGUCCGCCAU
Ppu01	UUGGAACUGCCCGCCCACTUGAG-GUCC	CGACCCUGCTCCAUCCAU
Ppu02	CCCGUGCTUGCCCGCCCAACGGUAA-GCGAG	CGAACCCUUGCAGAU
Ppu03	CCCGUGCTUGCCCGCCCAACGGUAA-GCGAG	UGAAGGUGUGU
Ppu04	CCCGGCTUGCCCGCCCACTUGAA-GCAACG	ACAACGGAUCCACACA
Rso01	CCUCCGCTUGCCCGCCCAACGGUAAACGGU	UCCCGCAGGUCCGUGCCAU
Sme01	CCGGGCTUGCCCGCCCAACGGUGG-UGGAGC	CAACAGCCACGGCACAAG
Sme02	CCGGCAGCTUG-CCCAACGGUGUAGAGCG	GACGUCUCCGCCAAAAGGCCUCUGAAUCUUCAGACCUUU
Sme03	UCCGACCGCAGCCCGCCCACTUGAAGCGU	CAGGGUCCGCCAUGCGCAUUGCGCGGAUUUCAUCCGCTUGGUGCGG
Sme04	CCGUGCTUGCCCGCCCACTUGAAGCGAU	CGUUGUUAUCCUUGUGCGGCAAGCGGCA
Sme05	CCGUGCTUGCCCGCCCACTUGA-GCGG	CGACCAAGUCCACGGAU
Sco01	CCGGGACTUG-CCCGCAGCGGUGA-GCGGG	AACGACCGCGGUGAUA
Sco02	CCGGGACTUG-CCCGCAGCGGUGA-GUGGG	AACGAAAGCGGUGAACA
Sco03	CCGGCAGCGUCC-CCCACTUGA-GCGGG	GACUCCACCCUUGCAGAC
Sco04	CCGGACTUG-CCCGCAGCGGUGA-AC	UUGCGUGCAUC
Sco05	CCGGGCTUGCCCGCCCACTUGA-AUCCGG	UAGUCCGCTUGCGCGGUGAAGCGA
Sfl01	CUAGACTUGA-CCCGCAGCGGUA-GGA	AAGGUGCGAUAUUGCGUUAUCCG
Son01	CUCCGACTUGCCCGCCCAACGGUAAAGGU	CACAGACCGCGCGCAUU
Son02	CCCGAAGCTUGAACCGGCACTUGA-GUAG	UUAAAGAACGCGGCUAGAUU
Sti01	CCCGGCTUGCCCGCCCACTUGAUGC	UGACGACCGCGUAAAGA
Sti02	CUCCGACTUGA-CCCGCAGCGGUA-GGA	AAGGUGAUAUGACAGGUAAGCA
Tma01	CCCGGCGGGG-CCCGCAACGGUGA-CGGGG	CACCAACCGCGCAGAAC
Tte01	CCCGGCGAGCCCGCCCACTUGA-GCGA	GGACCAAGCCGCUAGUA
Tte02	CCCGGCGAGCCCGCCCACTUGA-GCGA	GGACCAAGCCGCUAGUA
Vch01	CCCGGCTUGA-CCCGCAGCGGUA-GAGAG	AACCAACGCTCAAAC
Vvu01	CCCGAAGCTUGA-CCCGCAGCGGUAUAGAG	AACCAAGCTUUAUA
Xac01	CCCGGAGUCCCGCCCAACGGUGG-GCGAG	GUCAGGUGCCGCAACAG
Xax01	CCCGGAGUCCCGCCCAACGGUGG-GCGAG	GUCAGUUGCCGCAUAC
Ype01	CCCGGACTUGA-CCCGCAGCGGUAAGCGGA	AGUCACGGCGAUAGGUUUAAGAU
Aca01	CCAGUGCTUGCCCGCCCAACGGUAA-AAUUG	UAAACCAUAUUAAAGUUAUUAAGAUUA

FIG.41-36

Avi01	CCGUGCGUGCCCCCGCAACUGUGA-ACGG	CCAGCGAUGUCCAUCAU-----
Bfr01	CCCGGACAGU-CCCGCUGCUGAGAGCTCC	GUCUGAUUUCCCAUAA <u>CAAG</u> <u>GUU</u> -----
Bmg01	CCAGUACUGCCCCCGCAACUGUAA-GUGUG	GACGAACGAGUAA-----
Lma01	CCCGUGCUGCCCCCGCAACUGUAA-GCGAG	UGAAGCGUCAAU-----
Pfr01	CCCGAACUGU-CCCGCAGCGGUCA-AUGGG	AACGACACACCGUAAG-----
Rca01	CCCGACGCGCCCCCGCAACUGUACCGGA	GAGGGCGCGCGGAG-----
Rca02	CCGUGCGUGCCCCCGCAACUGUGA-GCGG	CGAGACGACGCGUGGAAG-----
Rca03	CCGUAACTGCCCCCGCAACUGUAA-GCGG	CCAGCAACCGCGCGCA-----
Rsp01	CCCGCGCGGG-CCCGCGCGUGUGA-CGG	GGAUUGCUCGCGGCAAGAG-----
Shi01	CCCGGCGUGCCCCCGCAACGGUAA-GCAGGUC	AGUCCGACGGCAACAAC-----
Sgi01	CCCGGACUGC-CCCGCAGCGGUGA-GUGGG	AACGACCGCGGUGAUA-----
Svi01	CCGAGACUGCCCCCGCAACUGUAA-CGGG	AGAGUCAUCCUCCU <u>UGAUGCU</u> <u>AUCUU</u> <u>ACGAUUUA</u> -----
Zmo01	CCUUGGCGUGCCCCCGCAACUGUAA-ACAGU	UGAAACCGCAAAA-----
Zmo02	CCAGUGCGCCCCCGCAACUGUAA-ACGG	CGACCAAGAUCAAAU-----

FIG.41-37

FIG. 41-38

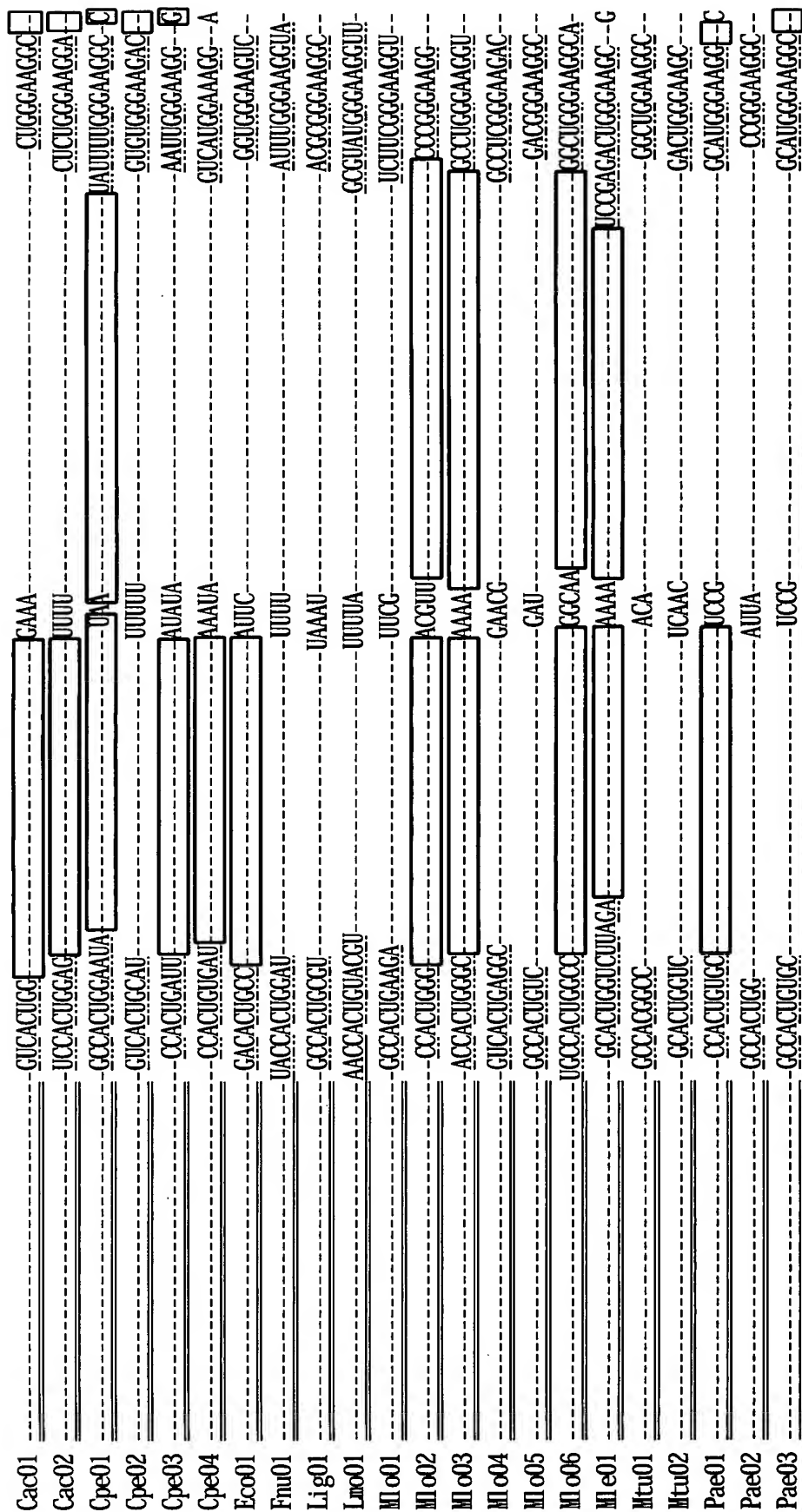


FIG.41-39



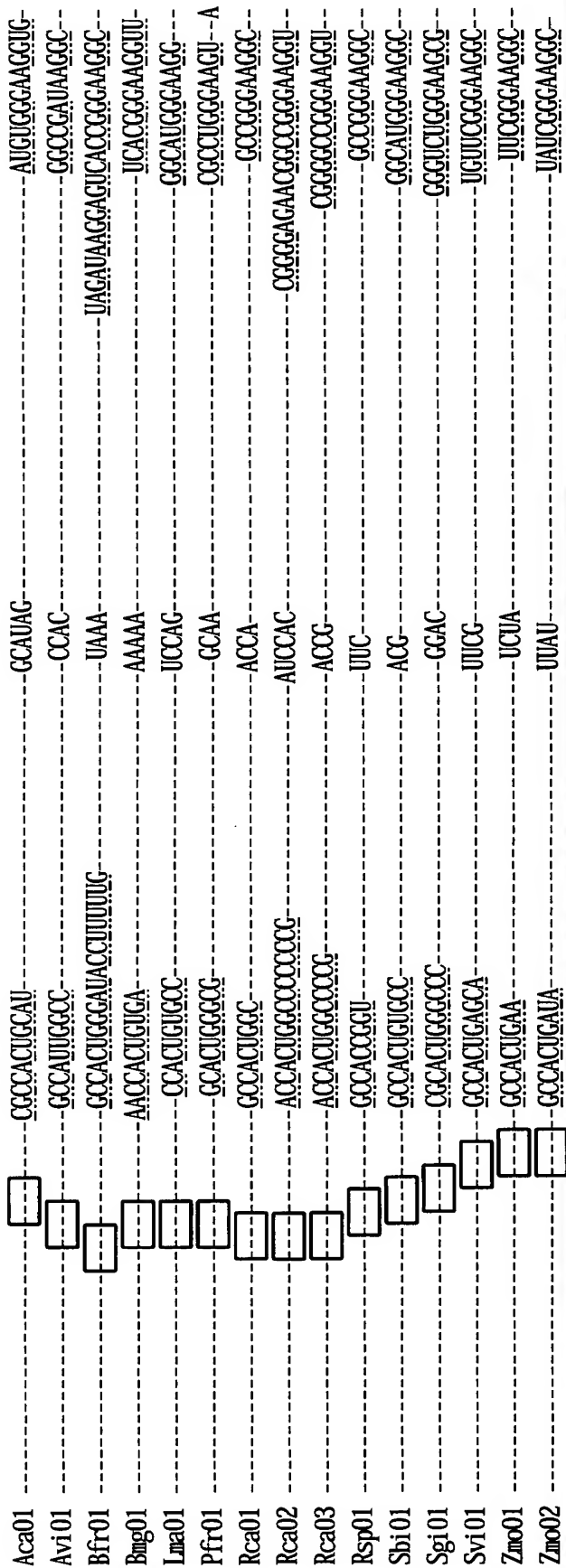


FIG.41-41

SS	y y	RAGYC	GRAGACC	GCC
Cons				
Atu01	GAUUGCAUGUUGUAG	CCCC	AAUUCAGCAGACCUUGCCUUGACGGCAAAUUGUCCACG	
Atu02	GAUACAGGACCGA	AAUCCGU	GAGCCAGCAGACCUUGCCUUGACAAAUUGGAACCAUCCG	
Atu03	UGCCCGAAUGUGUUCAGGUUUGAC	CCGU	AAGCCAGCAGACCUUGCCUUGACCGCAAAUUAUCCAUCCG	
Atu04	GCACCAAGCTUAGACC	CCG	AAGCCAGCAGACCUUGCCGGCAUAGAUAAAGUCCACAG	
Atu05	GAAGCGCGCAUGAA	CGU	UAGUCAGAGACCGGCCUUGCCAGAUAGACCGCAAC	
Atu06	CGUCACAGCGUGUUGAUA	CGCCG	AAGCCAGCAGACCUUGCCGUUUCAGCAAAAGCGUCU	
Bha01	UGUUGCAAUGUUGAC	CGUA	GAGCCAGCAGACCUUGCCUGUUCUAAACAGCACUGCUU	
Bha02	UUCUACUAGCUAA	AGCAC	GAGUCAGCAGACCUUGCCUUGACUUCACAAAGUUCGC	
Bha03	CACAUCCAGUGUUGA	UGUU	AAGUCAGCAGACCUUGCCUUAUUGUAUUGCACUUGCAC	
Bha04	GCAAGUACUUGCAUGAA	CAU	AAGUCAGCAGACCUUGCCUUCUUGAUUUGAGUGUGUAG	
Bsu01		GCCAA	GAGCCAGGAUACCUUGCCUUGUUGAUUCACACCAAAU	
Bj a01	CGCAGCAGCGCCGAUGA	CCAGC	AAGCCAGCAGACCGCCCGCCGACAAUAUAUUGGUCCA	
Bj a02	GGGAUUGCAAGGGAAACCCU	CUCCG	CAAGCCGGCAGACCUUGCCAGCGCGGACCAUUTUGGAC	
Bj a03	CGCAGAACCCACUGA	ACCCG	GAGCCAGCAGACCGGCCUUGCAUGUUCUUGACGCCAA	
Bj a04	GACCAAGUGUGACGAC	CCGC	GAGCCAGCAGACCUUGCCUUGACGCCUGGUGUACACGC	
Bj a05	CAGUUAAGGUAAAGCAG	CCGC	GAGCCAGCAGACCUUGCCUUGACGCCUGGUGUACACGC	
Bme01	CGAGCCAAAGCCAGAC	CCGC	AAGUCAGCAGACCUUGCCGUUUCGCGUACACCCAUUGCU	
Bme02	CCUUUAUCCCCAGAC	CCGC	GAGCCAGCAGACCUUGCCUUGUUGCAUUGAGCGCAUUGC	
Bme03	CAUGACCGCGAUUA	UCCGC	AAGCCAGCAGACCUUGCCUGUUCUUAAGUAGUCCAUUGU	
Bme04	GGCUGGAAGCGUUGA	CGGU	GAGCCAGCAGACCUUGCCUUGACCGUUGACCGUCCACG	
Ccr01	GGGACGGGUAGCAG	CCGU	GAGCCAGCAGACCUUGCCUUGCAGACAUAAAGUCCUCC	
Ccr02	GAGCCACAGAGCAUUGAC	CCGU	GAGCCAGCAGACCUUGCCGGCGGCGAGUUGUUAUUGCC	
Cte01	CGCCAGAUCC	GGCA	AAGUCAGAAAGACCUUGCCUUGAUUUUUUUGGCUUCCG	
Cte02	UUGGAGCGGUUUAU	CGCGU	AAGUCAGAGACCUUGCCACGUGAUCCAUUUGGACCAA	
Cte03	GGAAAGCA	GGGA	GAGUCAGAAAGACCUUGCCGUUAUUGCAGUAAUUGCUCC	
Cte04	UGCCCGAGGAAAGCUAAGUUAUUUUGA	GCCAUC	GAGUCAGCAGACCUUGCCGUUGAGUGUUGCCCGCGAAU	
Cte05	UGCAUCC	CCGU	AAAGUCAGCAGACCUUGCCAGUUAUCUUCUUGCUUGCGAA	

FIG. 41-42



FIG. 41-43

[illegible]

FIG. 41-44

Avi 01	GGACAAAGCCAGAC	CCGU	GAGCCAGGAGACCCUGCCGUAUAGCAUGGCCGGAAGC
Bfr 01	GUCCGAACAA	GCAGU	CAGUCAGAACACCCUGCCGCCUUAUCAAAGCCUGUUC
Bmg 01	CUCACGUAGAAUGA	UACAC	AAGUCAGGAGACCCUGUCUUAUUGAGGUUUGUUAU
Lma 01	UGAUGCUUUAACAGCCACGCGC	CUGGC	AAGCCCGGAGACCCGGCCCGGAAAUACAGAUACAA
Pfr 01	GUAGUGGAGGAAGUCCGGAGUGAUCUCCGAAUG	CCCAU	GAGUCCGAACACCCUGCCAGCAGCCACAACAUCUGUU
Rca 01	GGGGCACCCUGAGGGGACCCGCCUUGGA	UCCG	CAAGCCGGGAGACCCUGCCAGCGGAUGGAUUCGGGCG
Rca 02	GACCCGAGUUGAUCGAA	CCGC	AAGUCAGGAGACCCUGCCAUCCGCUUGGGGUGCGAAG
Rca 03	GGGGAAGCCAGCAG	CCGC	AAGUCAGGAGACCCUGCCAUCCGCUUCAACAACGCC
Rsp 01	GGCCGGGGGAGAGAA	CCG	GAGCCAGAACACCCGGCCUGACCCAGAGGUUCCCGCC
Sbi 01	CCUUGAGGUGGGUUGGCGCCACCC	GGCGGC	AAGCCCGGAGACCCGGCCCGGAGAGCCUACAGGUCCGGA
Sgt 01	ACGCCACUAGGUUUGUUGGCGGCGACAGUUG	CCCGC	GAGUCCGAACACCCUGCCCGCCUGCCGCAACCCGACCG
Svi 01	GCAGGACCGAUGAAGAC	CCCG	AAGUCAGGAGACCCUGCCGUAUCCAGUACACCCAUUGC
Zmo 01	GGUUGUUGGAU	CCUGU	GAGCCAGGAGACCCGACCCUUAUGUAUUGGUUCCAGCA
Zmo 02	UGAUGGAGCCCGUGAC	CCGU	CAAGUCAGGAGACCCUGCCUUAUAACCAAGUACAUCACU

FIG.41-45



NC\_003030.1/2824539-2824454 *AATCGTTAATATAGTTTAACTCATataT*. TTCTCGAatatgg. CAGGATgttttctacAAGGAA. ccTtaaa. TTTCTT. actaTCAGTGAATTGTGTTGTATGCA  
*Clostridium acetobutylicum*

NC\_003366.1/422828-422924 *TATGTACTTATATAAGTATATTCGtataTCCTCGACGatatgg*. GTTCAGTgttttctacTAGGAGGccGtaaaCAITCCTA. actaCGAATATATAGGTGATTTCIA  
*Clostridium perfringens*

NC\_003366.1/512410-512323 *TAAGTGTATTAATTTTAACTTCGtataTAATTCGTAatatgg*. TOCGAAAgtttctctacCTGCTAAccGtaaaATAGCAG. actaCCAGCAGTTCGTACTATATAAAT  
*Clostridium perfringens*

NC\_003366.1/2617892-2617807 *AAACCGGAATATAAACAAACCTCGtataA*. GCCTTCGataaagg. CAAGGCgttttctacCGGAAA. ccTtaaa. TTTCCG. TctaTCAGTGAATTTCATATATACTAT  
*Clostridium perfringens*

NC\_003454.1/1645257-1645173 *TAAATAATTTTAATAAAAAATTCGtataA*. GCCTAATatatgg. AAGGGTgtCCctacGGTTAA. ccAtaaa. TTAAOCAGctaCGAAAAATGTTTACTGTGCTT  
*Fusobacterium nucleatum*

NC\_002662.1/1159519-1159604 *GTCTATAATAGAACAACTTATTata*. ..CCTAGGatatgg. CTGGCGgttttctacCTCGTA. ccGtaaa. TGGCAG. acaaTAAGGAAATTCGATTTTTTAG  
*Lactococcus lactis* subsp. *lactis*

NC\_003210.1/610773-610679 *AATCCGCTACAATAATATAGTCGtataAGTTCGTAatatgg*. ACCGTTCgttttctctacCAGGCCAaccGtaaaATGCCAG. GctaCCAGCTATTTCTAAAAATTAAAT  
*Listeria monocytogenes* strain EGD

NC\_003210.1/1958601-1958511 *ATAACTTAAACCGAAATACTTCGtataATAGTTCGcat*. tgg. CCGACCAggttttctacCTCGTTAaccGtaaaTAACCCG. actaTCAGTACTTTCTGTATAAAGAAG  
*Listeria monocytogenes* strain EGD

NC\_004193.1/760480-760571 *CAATTTTATCCAATGCTTTTCGtataTCCTCGATAatatgg*. TTCCGAAAgTAtctctacCCGGTCAccGtaaaTGATCTG. actaTCAGGCGCAGAGCAGGTTCGG  
*Oceanobacillus iheyensis*

NC\_004193.1/769695-769781 *TCATCTAATTGAATAGAAAATGCGtataATTAAGCGGatatgg*. CCGACAGgttttctacCAGACCAccGtaaaTGGTTTG. actaCGCAGTAATTATATTGTATC  
*Oceanobacillus iheyensis*

NC\_004193.1/786775-786863 *CCGACAAATGCAAAATGAACCTCATataAATTTCAGAatatgg*. CTCAGAAgttttctacCCAGCA. ccGtaaaTGGCTCG. actaTCAGGGAAGATCGATCATTTTC  
*Oceanobacillus iheyensis*

NC\_004193.1/1103947-1104044 *AAACCTTATATATAGTTTTTTCATataATCGCGCGGatatgg*. CCTGCAAggttttctacCGGTTTaccGtaaaTGAACCCG. actaTCGAAAAAGCGGCAAAATTCGAT  
*Oceanobacillus iheyensis*

FIG. 41-46B

NC\_002745.1/430771-430861 GTTAAATAATTACATAAACCTCATatataATCTAAAGAtataggCTTTAGAAgttttctacCATGTTGccTtGaaCGACATG. actaTGAGTAAACAACACAATACTIAG  
Staphylococcus aureus subsp. aureus

NC\_004461.1/2432384-2432294 CATAAAATAATTATATATGACTCATatataATCTAGACAtataggCTTTAGAAgttttctacCGTGTGccAtaaaaCCACACCG. actaTGAGTAAACAATCCAAATACATT  
Staphylococcus epidermidis

NC\_004116.1/1093950-1093860 CAATTAAATATATGATTACTTATTTaT. GCTGAGgat.tgg.. CTTAGGgtCtctacAAGACA. ccGt. aa. TGTCTA. acAATAAGTAAAGCTAATAATAATAGCT  
Streptococcus agalactiae

NC\_002737.1/930757-930842 TGAATTCATAATGACATACTTATTTaT. GCCTGaat. tgg. . CCGACCGgtCtctacAAGACA. cc. ttaa. TGTCTA. acAATAAGTAAAGCTTTTAGGGCTTGC  
Streptococcus pyogenes

NC\_003028.1/1754791-1754878 AAAATTGAATATCGTTTACTTCTTTaT. CTCCTGaat. tgg. . CACGACgtTtctacAAGCTG. cc. Ggaa. CACCT. AacAATAAGTAAAGTCAGCAGTCAGAT  
Streptococcus pneumoniae

NC\_003869.1/586372-586463 AAAAATTTAATAGAGCACTCATatataTCCCGAGAtatgg. CTGGGAggtCtctacCGAACAAccGtaaaTTGTTGG. actaTGAGTGAAGTGTACCTAGCGG  
Thermoanaerobacter tengcongensis

Cosensus

.....<<<<<<<<.....>>>>>>>>.....<<<<<<<<.....>>>>>>>>.....>>>>>>>>.....

\*\*\*\*\*Y\*TWTA\*\*\*\*\*AT\*\*GG\*\*\*\*\*GT\*YCTAC\*\*\*\*\*CC\*\*\*\*AA\*\*\*\*\*YWAVR\*R\*\*\*\*

FIG.41-46C

**D. A-Box**

NC\_000964.1/626134-626051 AATTAAATAGCTATTATCATCTGtataACCTCAATaatatgg. TTTCAGGgtGtctacCAGGAA. ccGtaaaATCCTG. .aTtaCAAAATTTGTTTATGACATTT  
 Bacillus subtilis

NC\_003366.1/2870819-2870732 ATAAAAAATAAATTTTGGCTTGGtataACTCTAATGatatgg. ATTACAGgtGtctacCAAGAA. ccGAGaa. TTCTTG. aTtaCGAAGAAAGCTTATTTCCTTT  
 Clostridium perfringens

NC\_004460.1/504378-504467 GACTTTCGGCGGATCAACGCTTCatataATCCTAATGatatggTTGGCA. gtttctacCAAGAG. ccTtaaa. CTCTTG. aTTATGAAGTCTCTCGCTTATTCOG  
 Vibrio vulnificus

FIG.41-47

# E. Lysine riboswitch comparison

Command-1 Plain Text

Command-2 Base paired stem 1

Command-3 Base paired stem 2

1. Command-4 Base paired stem 3

Command-5 Base paired stem 4

Command-6 Base paired stem 5

ii. Command-7 Base paired stem 6

Command-8 Terminator poly-U

Command-9 Downstream AI stem paired to stem 1

Command-0 Optional base paired stem 2

cuag is 90% sequence similarity

2. CUAG is the Anti-Terminator

CUAG is the Terminator stem

1. Bha LysC AGUGAGGUAaggU-gcGAAACC--aAG-aguaC-ACAGUCUGAGAGAAUG----AGAUA----CGUUGAC----GACUGUUGGAagg--GGAUUCgcccgaadUGCAGUcGGGG-CUCAUCCG-AUUUGCGUggACCUAUUUJ---gaaUA-AGCAUAGGGcugucaCAACACUAG-----CCCCAA-----CUAGUGCUguggagAACuAUCUACGUJ
2. Bha dapA AGUGAGGUAaggU-gcGAAACC--aAG-agua--CACAUAUUGGA---GGA---GAUUGAGA---UCCGUUGAGAAUUGUG--GAAagg--GGAUUUgcccgaagCUGGAGAAUJ---CUCAU--GUUCUGAAGGCGUggUUCUGUAUJ---AaaUA-AAUACAGAAcugucaUAUAGCG-----GAUGU-----UGCUAUUAuggagGGcuAUCUCACGC
3. Bha nhaC AGAUGGGUAaggA-gcGGGUUUJ--aAG-aguaA-GCGUUG-----GAGGAUGACAACGAGGA-----UAAGCGC-CGAAagg--AAAACUGcccgaagCG-GAAGAUG--AGUCAAG-CGUCUUCUUGCUggGGUUGCAUJ---gaaUA-AAUGUAACAcugucaCAGC-----AGAUJ-----GCUGuggagAACUAACGUU
4. Bsu LysC GGUGAAGUAaggU-gcGAA-CUUC-aAG-aguaJ-GCCUUUGGAGAA-AGA-----UGGAU-----UCUGUGAA-AAAGCG-UGAAagg--GGAGCGUcGcccgaagCAAAUAAACC--CCAUC-GGUUAUUAUUUGCUggCCGUGCAUJ---gaaUA-AAUGUAAGGcugucaAGAA-----UCAU-----UUUCUuggagGGcuAUCUcGUUG
5. Cac LysA ACCUUUUGUAaggU-gcUUUAAGUC-aAG-aguaA-CGGUUUG--GAGUU-----GGCA-----AACUUAGAUGAACGG--UAAAgg-GGCUUUUAGccgaagCAUUUAGAUJ---GGCA---GAUUUAUUUGCUggCUUUUCAUA---CaaCA-UUAUGAUGGcugucaCUUUUAUUGUJ---UAGUU-----AUUAG--GUAGuggagCGcuACAA--GGU

FIG. 41-48A



6. Cpe\_nhaC    AAAGA-GGIagaggC-gCGAGAAUC-aAG-auua--CUAAAAUGGA---GUU-----AAGU-----AGCGUAGAGUUUAG--GAAagg--  
 GAUUUCgcccgaGUUUUGGCU-AAUACUUUA-GGCUAAUUGCUggGGUUGUAUA--gaaUA-UAUACACACugucCaCA-----AAA-----  
UGuggagAGCuAUCUCUUA
7. Cpe\_lysA    GACCAAAGIagaggU-gCGUAUU--aAG-agua--GUCAUAAGUAGCUGAC-----AAGU-----GUU--UUUUGUAUAU--GAAagg--  
 GAUUAGGccgaagAGAUUAU--GGUG---AUUAUAUUUCUGGUAUAUGUAU---aaU-AUGCAUAUACugucCaCUUJ-----GAAA-----  
 AAAGuggagUGcuACAGGUAC
8. Cpe\_lysP    AACUGAGAUagaggC-gCGAG-AUU-aU-agua--UCUUUGCAGAGGU-----AAGCA-----AUUGAAGCAAG-UGAAagg--  
 AUGAAUCgcccgaACCAU-UAGAAGAGGCUUAUAUUCUAUAGGUUggGGUUGCAUA--gaaUA-UAUGUAACCugucCaAAA-----UUUJ-----  
 UUUguggUgcuAUCUGA
9. Eco\_lysC    CAGGCCAGagaggC-gCG-U-UGCCCa---aguaACGGUGUUG---AGGA-----GCCAG-----UCCUGUGUAACACC-----  
 UggGGUGCAUCgcccgaGUAGUAGAGG-GCUGGCCA-CGUUCA-UCAUCgCUACAGGGG-CUgaaU--CCCCUG-  
 GGUgucCaCAGAGGCGUGCGAGUGGGGCUUUGCAAGUGGgaggCAcuUCCGGGUGA
10. Hin\_nhaC    UACAAAAGIagaggC-gcAAUUAU--aUA-agua--UUUUUUCAGAG-UG-----GAUAA-----CGAAGAAGAAAAA--GAAagg--  
 AAUAGUUGccgaAUCAAAAAA---GUCG---UUUUUUUGGUUgglUGCGUGGUGC--gaaA-GCG-GCGACCugucCaUAGUU-----UUUCUGAUU-----  
 AACUaggagUgcuACGGUUGU
11. Oih\_dapA    GUUUUGGAUagaggU-gCGAGAGC--aUC-agua--UAUACGCGGA---AGGG---AAUAG--CCCUAGUGAAGCGUAUG--GAAagg--  
 GGAUUCgcccgaCGAGU--GAAUACUCAUUA-ACUGGUUgglUGCGUUAUJ--gaaCAAAUAACAGUCCugucCaUAG-----GAGA-----  
 CUUAaggagGGcuAUCGAGCUG
12. Oih\_nhaC    UCGGUGGGIagaggA-gcAUAAC--aUU-agua--AUCGAC-----AAGAGGAUGACAACGAUGAUA-----GUUGU--GGAagg--  
 GUUGUUGccgaCA-UAUAAG--GGUACGA-CUUUAUAUUGCUgglUACAUUUJ---gaaUA-AAAGAUGCCugucCaUGCA-----AAAUUAG-----  
 UGCaggagAACUAUGAUGA
13. Ptm\_nhaC    UACUUGUGIagaggA-gcGAUCACU--aUA-agua--UUUUUUUGAG-UG-----GAUAA-----CGAAGAGGAAAAAG--GAAagg--  
 AGUGACGcccgaAUCAUUGAAA---GUCA---UUUUGAUUGGUUgglUGGCGUAUUC--gaaA-GGA-ACGUGCAUCugucCaUAGU-----CUUUUUUA-----  
 ACUAaggagCGcuACUGGUUGG

FIG. 41-48B

14. Sau\_1ysC    AUAUUUUGAUGaggC-gCAUCA-AUC-aUG-agua--AAGUUUAGA--UUA-----CUGUCUGC-----UAACAGCUGAAUUU--  
GAAagg·GUGCGAUGccgaagCGA-UUAUAAU--AGCA--GUUAUAUUUUUUUUggaACUUUUUUGGU--UaaGAGCU-GAGAGUuugucaUUAU--  
UAAA-----AAUAUaggagUGCAUCACUUUGUA
15. Sau\_1ysP    AAUUGAGUuagaggUUgCAUGUUUA--aUU-agua--ACUUGU-----CAGAAGUAUUUAUGGUACAUAAGUUUA--ACAAGU--  
GAAagg·UAAAGAUgcccgaAAUAGAUAUAA--ACCAUAAA--UUUAUUCUAUUggaGACAGUUU--CgaauA-GGAACUGUAcugucaCA-----GAA--  
-----UGUGAugUGcuA-C-CUUUAU
16. Sep\_1ysC    AGAUUUUGAUGaggC-gCAUCA-AUC-aUG-agua--AACUUUAGAUAUUUG--UCUGCUAA--CAA-UUA--UAGAGUU--AAAagg·G-  
UGAGAUgcccgaAAUGAUUCAUAAU--AGCA--GUUAUGAAUCGUUggaACUUAUUGGU--UaaGAGCUAU-AAAGUuugucaUUAU--AUUA-----  
---AUAUaggagUGCAUCACUUUGUA
17. Sep\_1ysP    AAUAGAGUuagaggUUgCAUUAUUA--aUG-aCUa--ACUUAU-----CAGAAGUCUAUGGACAUGUGUUA--AUAAGU--  
GAAagg·UAAUAUgcccgaAAUGAUGUUA-UUU-CCAU-AAAUAGCAUUgmuuGGAACAACUUU--CgaauA-GAAGUUGUAcuqucaC-----  
UUUA-----UGUGAugUGcuA-C-CUUUAU
18. Sf1\_1ysC    CAGGCCAGAAaggC-gCG-U-UGCCCa---aguaACGGUGUUGG--AGGA-----GCCAG-----UCCUGUGAUAAACAC--  
UGaggGGGUGCAUCgcccgaGdUGAUUGAACG-GCUGGCCA-CGUUCA-UCAUCgGUACAGGGG-CUGaaU--CCCCUG-  
GGUugucaCCAGAAAGGUUCGACAGUCGGCGUUUCGCAAGUGGgagACuUCUGGGUGA
19. Son\_1ysC    AGGAACAGAAaggA-gcGUUAA-CU-a--Ggua--GUCAAUCA--GGAG--CACAAA--CUCCAGCGAUUUGAU--  
GAGgg·AGAUUAGCgcccgaGgCAUAGAUUG--GUUGCUG-CAUGUUUAUGUGgGUUGCUUAGG-CUgaaU--CCUAACGAUuugucaCC-----  
UGUAUU-----GGuggagAGcuUCUGGUGAC
20. Son\_nhaC    CCUUUAAGUagaggC-gCGUGCCU--aUG-aCua--CUUGUGCG-----GAGGUGAUGCCGCAGA-----UGUACAAG--  
GAAagg·AGUCAGCcccgaagUAGC-CAGGU--CAUCA--ACCGAGC-GCUgGUUUUGCAU-CAAUaG--GUGCAAGACugCcaUAGU-----  
CAUC-----ACUAuggagCGcuACcUGAAGG
21. Tma\_asd    GACCCGA-CGaggC-gcGCCCGAG--aUG-agua--GGCUUGUCCC-----AUCAGGGGAGGAUUG--GGGACGGCU--  
GAAagg·CGAGGGCgcccgaagG-GUGCAGAGUUCUCCC-GCUCUGCAUGCCUgGGGUUUGGG--gaaUA-CCCAUACCAcugucaCGGAGG-----UC--  
-----UUCUCCGUGGagAGcCGAUUGGGU
22. Tte\_1ysA    AGGUGAGGUagaggC-gcGGGUCAUC-aAG-agua--ACAUGCCAGA--GGU--GUUAAG--GCCGAUGAAGGUGUGU--GAAagg-  
GGUG-CCCgcccgaagC-GCGUAAACUU-CCUUAAGGUUUACGCAGCUggaGCCUUAUGCC--gaaCA-GGUUAUAGGAcugucaCUGAAGGCU-----CCCCA-----  
GGCCUUCAGuggagAGcuAUCUGGCUA

FIG. 41-49A

[illegible]